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Regult
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
      Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478139 seqs, 66318000 residues
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594
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Maximum Match 100%
Listing first 45 summaries
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     Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB
                US-08-137-117D-86
US-08-436-717-86
PCT-US-96-1315-2-2
US-09-157-370-3
US-09-157-370-3
US-08-887-352B-9
US-09-20-005-10
US-09-716-028-10
US-09-716-028-10
US-09-716-028-10
US-09-716-028-13
US-08-466-151-9
US-08-466-151-9
US-09-109-207C-13
US-08-466-153B-13
US-08-466-153B-13
US-08-466-153B-13
US-08-466-153B-13
US-09-716-028-13
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Sequence 86, Appl
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 10, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 19, Appli
Sequence 2, Appli
Sequence 2, Appli
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	US-07-934-373C-39	US-08-579-378A-18	US-09-483-588-1	US-09L680-145-1	US-09-282-846-1	US-09-054-255-1	US-09-282-505-1	US-08-887-352B-8	US-09-025-403A-15	US-09-672-609-15	US-09-025-403A-17	US-09-672-609-17	US-10-113-996-7	US-09,-716-028-7	US-09-920-171-7			00-00-00/-00/0-/
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ALIGNMENTS

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US-08-137-117D-86

US-08-137-117D-86

JSequence 86, Application US/08137117D

Patent No. 5795965

GENERAL INFORMATION:

APPLICANT: SATO, KOA

APPLICANT: SATO, KOA

APPLICANT: BENDIG, Wary

APPLICANT: BENDIG, Wary

APPLICANT: SATO, KOA

TITLE OF INVENTION: INTERLEURIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESSEE: Poley & Lardner

STATES: JOO

STATES: JOOO K Street, N.W., Suite 500

CITY: Washington

STATES: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Plopy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Plopy disk

COMPUTER: DEAPLOATION DATA:

APPLICATION NUMBER: US-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08/137,117D

FILING DATE: 20-DEC-1993

CLASSIFICATION DATA:

APPLICATION NUMBER: US-08/137,117D

FILING DATE: 24-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US-08/137,117D

PRICH APPLICATION DATA:

APPLICATION NUMBER: 39-5476

FILING DATE: 25-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 25,258

TREERENCE/DOCKET NUMBER: 53466/126/AAOK

TELEPHONE: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 86:

ESCUENCE CHARACTER ISTICS:

LENGTH: 130 amino acids

TIPE: amino acids
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-137-117D-86
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US-08-436-717-86
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US-08-436-717-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 85.7%;
Best Local Similarity 90.1%;
Matches 100; Conservative
                                                                                                                                                                                                                                           PILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
PILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
APPLICATION NUMBER: JP 3-95476
PILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
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                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHAPED HUMAN ANTIBOD'
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                         NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 534
TELECOMMUNICATION INFORMATION:
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                                    TOPOLOGY:
                                                                                                                                        TELEFAX:
                                                                                                                                          TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                 TYPE:
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                                                                    130 amino acids
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JONES, Steven
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Pred. No. 2.7e-40;
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                                                                                                                       Matches
                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                            TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EF
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EF
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 805 Third
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                            ENGTH:
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61 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPWTFGQGTKVEIKRTV 114
                   61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114
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                                                                            1 DIQMTQSPSSLSASVGDRVTITTCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
                                                                                                                       98;
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                                                                                                                                       Similarity
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                                                            DIOMTOSPSSISASVGDRVTITCKASOSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPSRFSGSGSGTDFTFTISSLQPEDIATTYCQHSRENPYTFGQGTKVEIK 130
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                      82.5%;
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                                                                                                                                       Score 490; DB 5;
Pred. No. 2.9e-38;
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Pred. No. 2.7e-40;
2; Mismatches 9
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                                                                                                                         Mismatches
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                                                                                                                                                    Length 218;
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GENERAL INFORMATION:
APPLICANT: STEIPE, Boris
APPLICANT: STEINECHER, Stefan
APPLICANT: STEINECHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
FILE REFERENCE: P8341-8072
CURRENT APPLICATION NUMBER: US/09/157,370A
CURRENT FILING DATE: 1998-09-21
EARLIER FILING DATE: 1997-01-14
EARLIER APPLICATION NUMBER: PCT/EP95/02626
EARLIER APPLICATION NUMBER: PCT/EP95/02626
EARLIER APPLICATION NUMBER: DCT/EP95/02626
EARLIER FILING DATE: 1995-07-06
EARLIER FILING DATE: 1995-07-15
NUMBER OF SEQ ID NOS: 10
SOPTWARB: Patentin Ver. 2.1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-157-370-3
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Patent No. 5994511
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Best Local Similarity
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                                                          APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Ctaig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPAX: 650/252-94881
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                                       TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
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COMPUTER TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: ISM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acid
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco STATE: California
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85.8%;
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RESULT 7
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US-08-887-352B-10
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Patent No. 5994511
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Best Local Similarity 86.0%;
Matches 98; Conservative
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Henry B. TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Gence
1 DNA Way
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CITY: South San FI
STATE: California
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                                                                                                                                                                                                                                                                                         LENGTH: 114 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/887,352B FILING DATE: 03-Jul-1997 CLASSIFICATION: 530
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                                                                                       61 GVPSRPSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114
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                                                   GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIKRTV 114
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                                                                                                                                                                                                Score 486; DB 2; Length 114; Pred. No. 3.2e-38; 3; Mismatches 13; Indels
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Pred. No. 3.2e-38;
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US-09-109-207C-10
; Sequence 10, Application US/09109207C
; Patent No. 6172213

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RESULT 9
US-09-920-171-10
; Sequence 10, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
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; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-10
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US-09-296-005-10
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                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 10
LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 81.8
Best Local Similarity 86.0
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides FILE REPERENCE: PIL32CIr CURRENT APPLICATION NUMBER: US/09/296,005 CURRENT FILING DATE: 1999-04-21 EARLIER APPLICATION NUMBER: US 08/887,352 EARLIER FILING DATE: 1997-07-02 RARLIER FILING DATE: 1997-07-02 RARLIER FILING DATE: 1997-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial FEATURE: NAME/KEY: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                81.8%;
                                                                                                                                                                                                                                                                                                           Score 486; DB 3; Length 114;
Pred. No. 3.2e-38;
3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 486; DB 3;
Pred. No. 3.2e-38;
3; Mismatches 13
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US-09-716-028-10
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                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1

CURRENT APPLICATION NUMBER: US/09/716,028

CURRENT FILING DATE: 1000-11-17

PRIOR APPLICATION NUMBER: US 09/109,207

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/051,554

PRIOR FILING DATE: 1997-07-03

NUMBER OF SEQ ID NO 10

LENGTH: 114

TYPE: DET
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SEQ ID NO 10
LENGTH: 114
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                             Matches
                                                                                                                                                                                Query Match
Best Local Similarity
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CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR FILING DATE: 1999-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Improved Anti-IgE Antibodies (as FILE REFERENCE: P1123C2US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lowman, Henry B.
APPLICANT: Presta, Leonard G
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved
                                                                                                                                                                                                                                                                                 NAME/KEY: Artificial LOCATION: 1-114
                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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13
                       61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114
                                                                                                                                                           98;
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                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
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GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKVEIXRTV 114
                                                                               DIQLTQSPSSLSASVGDRVTITCRASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASYLES
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Pred. No. 3.2e-38;
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Pred. No. 3
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US-10-113-996-10

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TITLE OF INVENTION: Improved Anti-IgE Antibodies
FILE REFERENCE: P1122C3US
CURRENT APPLICATION UMMBER: US/10/113,996
CURRENT FILING DATE: 2002-04-01
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1997-07-02
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 09/920,171
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-887-352B-13
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US-10-113-996-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08887352B Patent No. 5994511
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Sequence 10, Appl
Sequence 10, Appl
No. 6761889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Henry
                                                         CLASSIPICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SVOBOda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P112
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lowman, Henry B. APPLICANT: Presta, Leonard
INFORMATION FOR SEQ
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                              SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/887,
FILING DATE: 03-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 114
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Local Similarity 86.0%;
hes 98; Conservative :
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                                         TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                  94080
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Lowe, John
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                                                                                                                                                                                                                                                                                                                                                                                                                            California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, VENTION: Improved Anti-IgE Antibodies and Method of VENTION: Improving Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                     USA
                    650/952-9881
                                         650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genentech, Inc.
                                                                                                                                                                                                                     US/08/887,352B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 486; DB 4;
Pred. No. 3.2e-38;
3; Mismatches 13
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Patent No. 6037453
GENERAL INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 81.8%;
Best Local Similarity 86.0%;
Matches 98; Conservative
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                                                 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-Jun-19
APPLICATION NUMBER: 08
FILING DATE: 15-MAR-19
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: 26-JAN-19
                                                                                                   NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044.
REFERENCE/DOCKET NUMBER: POT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-189
                                                                                                                                                                                               FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/74
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOPTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jardieu, Paula M
APPLICANT: Presta, Leonard
TITLE OF INVENTION: Immunog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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TOPOLOGY:
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               ENGTH: 218 amino acids
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                                                                                                                                                                                                                                                                                                                                 26-JAN-1994
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Pred. No. 6.8e-38;
3; Mismatches 13
                                                                                                                                           P0718P2C1D1
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ORGANISM: Artificial
FEATURE:
FEATURE:
FACTURE:
FACTURE:
FORMAN ARTIFICIAL
FORMATION: 1-218
FOTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13
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US-09-109-207C-13
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                                                                                                                                                                       Sequence 13, Application US/09296005

Patent No. 6299957

GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P1123C1r
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26

SEQ ID NO 13
LENGTH: 218
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
PRIOR FILING DATE: 1998-06-03
LENGTH: 218
TWODE: DET
Query Match
Best Local Similarity
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Best Local 9
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ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Artificial
LOCATION: 1-218
COTHER INFORMATION: Light chain sequence derived from MAB11
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61 GVPSRFSGSGGGTDFTLTISSLQPEDFATYYCQQSHEDFYTFGQGTKVEIKRTV 114
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Score 486; DB 3;
Pred. No. 6.8e-38;
                    Length 218;
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        61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114
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Search completed: December 29, 2004, 19:37:36 Job time: 28.3991 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	თ	ហ	4	ω	N	-	Result
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Adl93655 Human CD4	Abb74900 Humanised	Aaw90931 Humanised	Aab45996 Human MUC	Adn07034 Anti-IgE	Aab76947 Full vari	0	Aaw95658 Mus muscu	Adn07031 Anti-IgE	Aab76944 Variable	Aaw95655 Mus muscu	Aaw95654 Mus muscu	Aaw13922 Light cha	Aab45995 Human MUC	Abb74901 Humanised	Aaw90932 Humanised	Abb74899 Humanised	Aaw90930 Humanised	Adl92462 Single do	Abp96011 HSA antib	Aaw13563 Humanised	Aaw22842 Human ant	Aam49204 Humanised	Aar85242 Humanised	Humanis	Description

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Ad192461	Abp96010	Ad192369	Abj38594	Abp95997	Aab45994	Aab46005	Aab46006	Aab46008	Aab46038	Aab46007	Aay02472	Adn07066	Adn07030	Aab76943	Ado36372	Ad192386	Ad191345	Abp96009	Aab46010
Single do	HSA antib	Human pha	Hepatitis	Human ser	Human MUC	Human MUC	Human MUC	Human MUC	Human TF	Human MUC	A single	F(ab)-pha	Anti-IgE	Variable	Intracell	Anti-HSA	VL chain	HSA antib	Human MUC

ALIGNMENTS

RESULT 1 AAE28148

AAE28148 standard; protein; 114 8

AAE28148;

27-DEC-2002 (first entry)

Humanised 9F3 version 13 (V13) light chain variable domain.

Human; interferon alpha; IFNalpha; insulin-dependent diabetes mellitus; autoimmune disease; systemic lupus erythematosus; autoimmune thyroiditis; antibody therapy; immunosuppressive; antiinflammatory; dermatological; 9F3 monoclonal antibody; light chain variable domain.

Homo sapiens.

Synthetic.

Location/Qualifiers 2438 /note= "Complementarity determining region 1 (CDR1)" 5460 /note= "Complementarity determining region 2 (CDR2)" 0		FT Region	PT	FT Region	PT	Ş
y determining region 1 (CDR1)" y determining region 2 (CDR2)" y determining region 3 (CDR3)"		_				•
region 1 (CDR1)" region 2 (CDR2)" region 3 (CDR3)"	/ determining		/ determining		/ determining	
(CDR1) " (CDR2) "	region 1		region 2		region 3	
	(CDR1)"		(CDR2) "		(CDR3) "	-

WO200266649-A2

29-AUG-2002.

29-JAN-2002; 2002WO-US002709

22-FEB-2001; 2001US-0270775P. 09-JAN-2002; 2002US-00044896.

(GETH) GENENTECH INC.

Chuntarapai A, Kim JK, Presta LG, Stewart T;

WPI; 2002-682767/73.

CX8X777X8X7X8X8X8X8X8X8X New anti-interferon alpha monoclonal antibody, 9F3, useful for treating autoimmune diseases e.g. insulin-dependent diabetes mellitus, systemic lupus erythematosus and autoimmune thyroiditis.

Disclosure; Page 97; 100pp; English.

The present invention relates to novel anti-interferon alpha (IFNalpha)

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Matches
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Best Local
Antibodies (Ab) comprising a humanised variable region specifically binding to a varicella zoster virus (VZV) can be used to treat or prevent VZV infection. They may optionally be attached to a therapeutic agent. They may also be used, when labelled, to detect VZV particles and infected cells in blood; for the removal/ neutralisation of infectious VZV in blood; for the selection/ isolation of human monoclonal Abs and for the design of (non-) peptide mimetics with similar diagnostic and therapeutic uses. The variable region CDR portion is derived from murine Ab 206 and the heavy and light chain variable region frameworks are NEWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monoclonal antibody, 9F3 which binds to and neutralises a biological activity of IFN-alpha subtypes. The anti-IFNalpha monoclonal antibodies of the invention are useful for treating autoimmune diseases such as insulin-dependent diabetes mellitus, systemic lupus erythematosus and autoimmune thyroiditis. They are useful as reagents in diagnostic assays for IFN-alpha expression, for the affinity purification of various IFN-alpha expression, for the affinity purification of various in the detection of IFN-alpha in diagnostic assay methods. Sequences of the invention are also useful in antibody therapy. The present sequence is anti-luman IFNalpha monoclonal antibody 9F3 version 13 (V13) light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; varicella zoster virus; Ab; VSV; treatment; prevention; infection; detection; isolation; monoclonal antibody; MAb; mimetic; humanised; murine; heavy chain; light chain; variable region; CDR; NEWM;
                                                                                                                                                                               Claim 7; Page 31; 58pp; English
                                                                                                                                                                                                                                   Varicella zoster virus gpIII antibody with humanised variable region for treatment, prevention or diagnosis of varicella zoster virus
                                                                                                                                                                                                                                                                                             WPI; 1996-010932/01
                                                                                                                                                                                                                                                                                                                               Мовв МТ,
                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1994;
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                                                                                                                                                                                                                                                                                                                               Wallace TP,
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                                                                                                                                                                                                                                                                                                                                                                  BIOPHARMACEUTICALS INC.
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody; mAb; humanised; murine; mouse; 5c8; hu5c8; light chain; anti-CD145; CD145-antibody complex; 3D structure; three dimensional structure; drug design; drug discovery; activated T cell; CD40 interaction; T cell dependent immune response; agonist; antagonist; immune response; inflammatory response; autoimmune disease; allergy; inhibitor response; organ graft rejection; B cell cancer; Alzheimer's disease; multiple sclerosis; antiinflammatory; immunosuppressive; antiallergic; cytostatic; dermatological; antiasthmatic; nootropic; neuroprotective; antiarteriosclerotic; antiriviral; antidabetic; cardiant; antischaemic; vasodilator; antirheumatic; antiarthritic; antipsoriatic; immunomodulator; antibody; complementarity determining region; CDR; protein co-ordinate data.
                                                                                                                                                                                                                                                                   Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and REI respectively. The framework may include at least one mutation that improves binding specificity or affinity. The heavy and light che variable regions are preferably (VZVHu-VH, -VHKFIIS, -VHTLY, -VHKVRSE -VHS) and VZVHuVK respectively
                                                                                                                                                                                   Binding-site
                                                                                                                                                                                                                                             Region
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28-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM49204 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 111
                                07-MAR-2002.
                                                                                        Binding-site
                                                                                                                           Region
                                                                                                                                                              Region
                                                                                                                                                                                                          Binding-site
                                                                                                                                                                                                                                                                                                       Chimeri
                                                                                                                                                                                                                                                                                                                  Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIK
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31. .32
                                                                                          95.
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                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                   /label= CDR3
/note= "Complementarity
                                                                                                                                    label= CDR2
note= "Complementarity
                                                                                                                                                                                                note=
                                                                                                                                                                        note= "Binds
                                                                                                                                                                                                                                 label= CDR1
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                                                                                                                            .101
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                                                                                           . 96
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                                                                                                                                                                                                                     "Complementarity determining
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                                                                             "Binds to
                                                                                                                                                                                                "Binds
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                                                                                                                                                                                                                                                        part of the crystal of the invention"
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                                                                               CD145
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                                                                               (AAM49202)
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31-AUG-2001; 2001WO-US027352

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RESULT 4
AAW22842
ID AAW2
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AC AAW2
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AC AAW2
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AC 12-S
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                                                                                                                                                                                                                                                                                                                                                                                                                        CC complex with an anti-CD45 antibody or its antigen-binding fragment, and cches tructure coordinates of such a crystal. In particular, the crystal comprises human CD145 (AAM49202) and a humanised version of the murine commoncional antibody 5c8 (husce; AAM49202) and a humanised version of the murine commoncional antibody 5c8 (husce; AAM49202). CD145, also known as CC CD401, gp39; T-BAM, 5c8 antigen, CD40CR and TRAP) is a 32 kD type II CC membrane glycoprotein which is transiently expressed on activated T CC cells. It interacts with CD40 which is expressed on mature B cells, CC macrophages, dendritic cells, fibroblasts and activated endothelial CC cells. This CD40:CD145 interaction is required for T cell-dependent CC antibody responses, type I T-helper cell responses, and nitric oxide (No) CC production by macrophages, and disruption of the CD40:CD145 interaction via the use of an anti-CD145 antibody has been shown to reduce the cof the invention can be used to determine the three dimensional structure of the CD145 anti-CD145 antibody complex, and thereby provide information CC about this interaction which may be of use in designing non-antibody CC 19145 agonists and antagonists which modulate the CD40:CD145 interaction. CC Such compounds may be used in the treatment of an unwanted immune cC asthma, chronic obstructive pulmonary disease (no antibody because, treat systemic consentive, pulmonary disease (no compounds may be used in the treatment of an unwanted immune cC asthma, chronic obstructive pulmonary disease (no compounds may be used in the treatment of an unwanted immune cC asthma, chronic obstructive pulmonary disease (no compounds may be used to a therapsutic agent, rejection of a C cantibody, and inhibitor response to a therapsutic spent; respectively, the medical consense, lumpus neuritis, cc sendance of a consense of a co
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Best Local S
Matches 91
    12-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-SEP-2000;
16-MAR-2001;
                                         AAW22842;
                                                                              AAW22842 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-329760/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 8; 470pp; English.
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                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                            91;
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                                                                                                                                                                                                   GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV
                                                                                                                                                                                GVPARFSGSGSGTDFTLTISSVEPEDFATYYCQHSWBIPPTFGGGTKLBIKRTV
                                                                                                                                                                                                                                                           DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                        218
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5c8 (hu5c8). (Updated on 29-AUG-2003 to standardise OS
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2001US-0276452P.
  (first entry)
                                                                              protein; 132
                                                                                                                                                                                                                                                                                                                                                        83.2%;
79.8%;
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Pred. No. 2e-25;
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Best Local
L-selectin; humanised antibody; HuDreg 55; acute organ damage; organ failure; poly-trauma; haemorrhagic-traumatic shock.
                                                                                                                                                                                                                                                                                                                                                                  (MAb) light chain variable region, useful in medicine, pharmacology and biochemistry. The isotype of a MAb secreted by the human/human hybridoma HT was determined to be mu and kappa. Human MAb was purified, and the antigen recognised by human MAb CLN"-IgM identified by western blotting
                                      Humanised
                                                             17-OCT-2003
03-JUN-1997
                                                                                                    AAW13563;
                                                                                                                           AAW13563 standard;
                                                                                                                                                                                                                                                                                                                                           Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a human anti-tumour antigen monoclonal (MAb) light chain variable region, useful in medicine, pharmaco
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 11; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anticancer human monoclonal antibody variable region sequences related DNA and RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-276726/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-1995;
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                                                                                                                                                                                                                                                                                           97;
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                                                                                                                                                                                                     GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                       DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
                                                                                                                                                                                        GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPQTFGQGTKVEIKRTV
                                                                                                                                                                                                                                          DIOMTOSPSSLSASVGDRVTITCRASOSIS----SYLNWYQOKPGKAPKLLIYAASSLOS
                                    anti-L-selectin antibody HuDreg 55 light chain.
                                                                                                                                                                                                                                                                                           Conservative
                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95JP-00278266
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/label=_CDR_2
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                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                     83.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    = mat_peptide
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                                                                                                                                                                                                                                                                                         Score 493; DB
Pred. No. 1.6e
8; Mismatches
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l.6e-25;
les 5;
                                                                                                                                                                                                                                                                                                                 Length 132;
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RESULT 6
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XC ABP9
XC ABP9
XX ABP9
XX ABP9
XX Liga
XX Liga
XX Liga
XX anti
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Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised anti-L-selectin antibody HuDreg 55 comprises 2 light chains each having the sequence given in AAW13563 and 2 heavy chains each having the sequence given in AAW13564. These are encoded by the cDNA clones given in AAV61280 and AAV61281. HuDreg 55 can be used to prevent multiple organ failure associated with polytrauma and for the prevention of acute organ damage associated with extracorporeal blood circulation. The antibody inhibits interaction between the carbohydrate-recognising domain of the selectin and the corresponding cell surface receptor. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-1995;
19-SEP-1995;
27-DEC-1995;
                                                                  Ligand; human serum albumin; HSA; antibody; cytostatic; anti-HIV; antiinflammatory; antianaemic; immunosuppressive; neuroprotective; dual-specific ligand; cancer; HIV infection; hepatitis; rubella; inflammation; autoimmune disorder; multiple sclerosis; Crohn's dis
                           Homo sapiens
                                                     myasthenia gravis.
                                                                                                                                                                     01-MAY-2003
                                                                                                                                                                                                                            ABP96011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck A,
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                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                        antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1997-165036/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-selectin antibody to prevent acute organ damage and failure - during extracorporeal circulation or following rauma, e. g. haemorrhagic-traumatic shock.
                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                            98;
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BOEHRINGER
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                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                              GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                     DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
                                                                                                                                                                                                                                                                                                                                                    DIOMTOSPSSLSASVGDRVTITCKASOSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,
                                                                                                                                     related Vkappa chain
                                                                                                                                                                    (first entry)
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95EP-00114696.
95US-00578953.
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GER MANNHEIM
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                                                                                                                                                                                                                         protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                      86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52pp; English
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                                                                                                                                                                                                                                                                                              SSLQPEDFATYYCQQSNEDPWTFGQGTKVEIKRTV
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 490; DB 2;
Pred. No. 3.7e-25;
4; Mismatches 12
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                                                                                                                                                                                                                                                                                                                                                                                                           12;
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disease;
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RESULT 7
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(C) (a) a first single immunoglobulin variable domain with a binding

(C) specificity to a first antigen or epitope; and (b) a second complementary

(C) immunoglobulin single variable domain with a binding activity to a second

(C) complementary to a second domain single watiable domain with a binding activity to a second

(C) complementary, and

(C) complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADL92462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIQMTQSPSSLSASVGDRVTITCRASQSVS----SYLNWYQQKPGKAPKLLIYLASRLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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A
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
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Pred. No. 2
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antirheumatic; antiarthritic; antiasthmatic; antiallergic; antibacterial; virucide; immunosuppressive; antidiabetic; neuroprotective; muscular; dermatological; gene therapy; inflammatory; rheumatoid arthritis; asthma; Crohn's disease; allergic hypersensitivity; bacterial; viral infection; autoimmune disorder; type I diabetes; multiple sclerosis; myasthenia gravis; systemic lupus erythematosus; cancer; light chain variable region; human; E5sd.

Single domain antibody-related light chain variable region

E58d

protein.

56 60

immunoglobulin single variable domain; cytostatic; antiinflammatory;

Unidentified

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel dual-specific ligand comprising a first C immunoglobulin single variable domain having a binding specificity to a C first epitope or antigen and a second complementary immunoglobulin single variable domain having a binding specificity to a CC first epitope or antigen and a second complementary immunoglobulin single CC variable domain having a binding activity to a second epitope or antigen. CC antirheumatic, antiarthritic, antiasthmatic, antiallergic, antibacterial, cC virucide, immunosuppressive, antidiabetic, neuroprotective, muscular and CC dermatological activities and may be useful in gene therapy, ligand CC binding assays or for diagnosing, preventing or treating a disease CC selected from an inflammatory disease such as rheumatoid arthritis, CC asthma or Crohn's disease, an allergic hypersensitivity, a bacterial or viral infection, an autoimmuné disorder such as type I diabetes, multiple sclerosis, myasthenia gravis or systemic lupus erythematosus or cancer. The current sequence is that of a single domain antibody (dab)-related control of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 96
nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
                                                                                  Pas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antitheumatic; anti-Fas;
                                                                                                                                                              Humanised anti-Fas designed light chain Leu 1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New dual-specific ligands, useful in drug discovery and development, for diagnosing, preventing or treating a disease, such as cancer, autoimmune disease, or inflammatory disease, including rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUN-2002;
27-DEC-2002;
                                                                                                                                                                                                                                                                     AAW90930 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arthritis or asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Winter G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2003; 2003WO-GB002804.
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                                                                                                                                                                                                                                                                                                                                                                                       GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                      DIQMTQSPSSLSASVGDRVTITCRASQSVS----SYLWWYQQKPGKAPKLLIYLASRLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
                                                                                                                                                                                                                                                                                                                                                                  GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQNWWLPPTFGQGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 3; 174pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 489; DB 8;
Pred. No. 2.4e-25;
6; Mismatches 6
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RESULT 9 ABB74899

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This invention describes a novel humanized anti-Pas antibody-like CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas CC ligand system, by binding to Fas on the cell surface, and prevents CC apoptosis in cells with a normal system, by inhibiting binding between CC Pas and its ligand. The products of the invention have anti-inflammatory, CC anti-nemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, CC antirheumatic, nephrotropic, anti-infertility, neuroprotective, CC diseases associated with the Fas/Fas ligand system, especially systemic CC lugus erythematosus, Hashimoto disease, rheumatoid arthritis, graft CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic CC unti-percent disease, scleroderma, Goodpasture syndrome, Crohn's CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, CC cardiomyopathy, glomerulomephritis, hepatitis (filminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic contended in the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody light chain construct designated Leu 1 cc which is described in the method of the invention
                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1998;
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                                                                                                                                                                                                                                                                                           Similarity
GVPSRPSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTV
                                                                                                                                                                     DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
                                                            GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCOHSWGIPRTFGQGTKVEIKRTV 114
                                                                                                                            DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMWYQQKPGKAPKLLIYAASNLBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 156-157; 263pp;
                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                      Score 489; DB 3;
Pred. No. 4.7e-25
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standard;

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RESULT 10
AAW90932
ID AAW90
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AC AAW90
XC AAW90
XX
DT 08-AU
CX
DT 08-AU
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CX
DE Humar
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CW Fas;
KW Fas;
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          Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-ratic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; anti-ras; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; mouse; humanised anti-Fas antibody; Fas/Fas light chain subunit; apoptosis; immunosuppressive; autoimmune disease; allergy; atopic.
                                                                                                                    08-AUG-2000
                                                                                                                                                                           AAW90932 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing humanized anti-Fas antibody, used ting autoimmune diseases, allergy, and atopy.
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                                                                                                                                                                                                                                                    81
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                                                                                                                                                                                                                                                                                                                                                                                                                                238 AA;
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Pred. No. 4.7e-25;
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lupus erythematosus;
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antiallergic;
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GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTV GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114 21

DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES

PSSLSASVGDRVTITCKASQSVDYDGDSYMWYQQKPGKAPKLLIYAASNLES

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CC molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas CC ligand system, by binding to Pas on the cell surface, and prevents CC apoptosis in cells with a normal system, by inhibiting binding between CC Pas and its ligand. The products of the invention have anti-inflammatory, CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, cimmunomodulatory, dermatological, immunosuppressive, thyromimetic, CC antiarteriosclerotic, cardiant and hepatropic activity. (1) induce approved by binding to cell surface Pas or inhibit it by competitive CC inhibition of ligand binding. (1) are used to treat and/or prevent CC diseases associated with the Pas/Fas ligand system, especially systemic CC upus erythematosus, Hashimoto disease, rheumatoid arthritis, graft CC versus host disease, soleroderma, germicious or hypoplastic CC anemia, Addison's disease, soleroderma, Goodpasture syndrome, Crohn's Cdisease, autoimmune hemolytic anemia, sterility, mysathenia gravis, CC disease, autoimmune hemolytic anemia, sterility, mysathenia gravis, CC ardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral CC (B, C or D) or alcoholic), and transplant rejection. (1) selectively cills. They bind to both human and murine Pas, so can be evaluated in murine disease models. (1) act on the active site of Pas, i.e. they mimic CC inducing a human anti-murine antibody response. This sequence represents ca humanised anti-Pas antibody light chain construct designated Leu 3 which is described in the method of the invention
                                        Query Match
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                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hashimoto disease; rheumatoid arthritis; graft versus host disease;
Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 161-162; 263pp; English.
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                       Local
   Similarity
97; Conserv
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     Conservative
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98JP-00276882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a novel humanized anti-Fas antibody-like
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Score 488; DB
Pred. No. 5.4e
5; Mismatches
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                   488;
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                   DB 3;
5.4e-25;
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                                        Length 238;
     Indels
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RESULT 12
AAB45995
ID AAB45
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AC AAB45
AC AAB45
AC AAB45
XX
XX
DT 23-MA
XX
XX
XX
DB Human
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AM
MUC1;
KW MUC1;
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ABB74901
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N-PSDB; ABL45941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand; light chain subunit; apoptosis; immunosuppressive; antiallergic; autoimmune disease; allergy; atopic.
MUC1; human; vaccine; conformation-dependent antigen; antibody; of antidiotypic antibody; cytostatic; virucidal; antibacterial; TF
                                              Human MUC-1
                                                                                                                                        AAB45995 standard; peptide, 240 AA
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 14 (Preparatory); Page 94; 194pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drug containing humanized anti-Fas antibody, used for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-2000; 2000JP-00090918
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                                                                            23-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKVEIKRTV 134
                                                                                                                                                                                                                                   GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                             DIVLTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMMWYQQKPGKAPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                       238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    atopy and
                                              scFv clone R2.
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                           (first entry)
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85.1%;
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Pred. No. 5.4e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CC of an antidiotypic antibody (AD2) or another peptide which: (a) encode a region of specifically binds to the binding size of an antibody (AD1) or an antigen CC binding molecule; and (b) immunologically mimics the initial antigen. The cepitope is partially or completely conformation-dependent, and has an ciden. (I) is used in the form of linear or circular naked DNA and/or caids. (I) is used in the form of linear or circular naked DNA and/or cident. (I) a corresponding vaccine (V2) against antigens which care not proteins or peptides, as defined above but which have epitopes which show an immunogenic structure; (2) preparing (V1) and (V2); (3) CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3) CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3) CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3) CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3) CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3) CC which show an induction structure; (3) preparing (V1) and (V2); (3) CC which show an induction of structure; (4) MUC1-conformation epitope confined the specification; (5) antidotypic antibody fragments against the TF confirmation one of 24 approximately 200 residue amino acid sequences, all fully defined in the specification; (6) TF carearbohydrate epitope mimetics conformation; and (7) DNA sequences encoding the fragments and confirmed in feetined in (3, 4, 5, or 6). (V1) and (V2) are used to treat cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria and parasites. The vaccines are effective in cases where vaccination has confirmed in the specification and confirmed in cases where vaccination has previously not been possible
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel vaccine (V1) against conformation-dependent antigens (CDA) comprising DNA (I) and/or an antibody, or peptide which immunologically inmitates CDA, is new. (I) encodes a rof an antiidiotypic antibody (Ab2) or another peptide which: (a) specifically binds to the binding site of an antibody (Ab1) or an analysis of the binding site of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-049937/06
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09-SEP-1999;
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                                                                                         133
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                                                                                                                                                                                                                                         96;
                                                                                                                                                                                                                                                                                Similarity
                   GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKR 112
                                                                                         DIQMTQSPSSLSASVGDRVTITCRASQSIS----SYLNWYQQKPGKAPKLLIYHASFLQS
                                                                                                                                DIQMTQSPSSLSASVGDRVIITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES 60
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99DE-01043016
                                                                                                                                                                                                                                                                            82.2%;
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                                                                                                                                                                                                                                                                            Score 488; DB 4;
Pred. No. 5.5e-25;
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                               Length 240;
                                                                                                                                                                                                                                         Indels
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody; heavy chain; light chain; variable region; human; monoclonal; complementarity determining region; human; adr type hepatitis B virus; HB virus; CDR; virus antigen; anti-HB antibody; vaccine.
                                                        Mus musculus
                                                                                                         eczema; anaphylactic shock; urticaria.
                                                                                                                                        atopic
                                                                                                                                                                  histamine;
                                                                                                                                                                                        Variable light chain;
                                                                                                                                                                                                                                                 Mus musculus anti-IgE e426 variable light chain.
                                                                                                                                                                                                                                                                                                          08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                   AAW95654 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibody. It can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997-140911/13
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                                                                                                                                  ine; production; hypersensitivity; allergen; anaphylaxis;
allergy; asthma; allergic rhinitis; conjunctivitis; hay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     بر
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPSRFSGSGSGTDFTLTISSLQPEDPATYYCQHSWGIPRTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 10-11;
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                                                                                                                                                                                           IgE;
                                                                                                                                                                                        antibody; anti-IgE; reduction; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus antibody
                                                                                                                                                                                                                                                                                                                                                                                                                   114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 486; DB 2
Pred. No. 4e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 114;
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RESULT 15
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                                                                                                                                                                                             Variable light chain; IgB; antibody; anti-IgB; reduction; prevention; histamine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Improving affinity of polypeptides, particularly anti-IgE antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                                                                                                                                                                        08-JUN-1999
                                                                                                                                                                                                                                                                                                                                           AAW95655 standard;
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            Lowman HB,
                                                                                       30-JUN-1998;
                                                                                                                  14-JAN-1999.
                                                                                                                                           WO9901556-A2
                                                                                                                                                                      Mus musculus
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                                    (GETH ) GENENTECH INC.
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          Presta LG,
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Pred. No. 4
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            Lowe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Improving affinity of polypeptides, particularly anti-IgE antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                                                                                                                                                                                  Sequence 114 AA;
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                                                                                                         61
                                                                                                                                              ch 81.8%;
1 Similarity 86.0%;
98; Conservative :
                                                                     GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVBIKRTV 114
                                                                                                                                                                                                                       Score 486; DB 2; Length 114; Pred. No. 4e-25; 3; Mismatches 13; Indels
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2: pir2:*
3: pir3:*
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                       g kappa chain v-y
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BOUDDERKKKKKKUUR

Query Match Best Local ! Matches 9!	,ACCEBSION: S40331 ,Status: preliminary; translat: ,Molecule type: mRNA ,Residues: 1-123 <klb> ,Cross-references: EMBL:X72441 ,Superfamily: immunoglobulin V ,Keywords: heterotetramer; immun,32-106/Domain: immunoglobulin</klb>	;Date: 06-Mar-1994;Accession: \$40331;Klein, R.; Jaeniclaur. J. Immunnol. 23;Title: Expressed;Reference number:	BSULT 1 (40331 'g kappa chain - human 'Species: Homo sapiens		444	42		39				,			
ch l Sim: 95;	n: \$4031 preliminary type: mRNA : 1-123 <kl: :="" el="" ferences:="" heterotet:="" ily:="" immu<="" immuno="" main:="" td=""><td>Mar-1: : S40: ; Jae: unol. press</td><td>ain -</td><td></td><td>433 433 432.5</td><td>433</td><td>434</td><td>436 435</td><td>437</td><td>437</td><td>437</td><td>438</td><td>438</td><td>438</td><td></td></kl:>	Mar-1: : S40: ; Jae: unol. press	ain -		433 433 432.5	433	434	436 435	437	437	437	438	438	438	
81. Similarity 85.)5; Conservative	inary; ti mRNA RLES ss: EMBL mmunoglol rotetrame immunog	06-Mar-1994 #sequence_revisi ion: S40331 R.; Jaenichen, R.; Zachau, Immunol. 23, 3248-3271, 1993 Expressed human immunoglobu nce number: S40312; MUID:940			72.9 72.9 72.8		•	73.4 73.2	73.6		73.6	•	•	73.7	
81.3%; 85.6%; ative	cansla x724 pulin ar, in lobul:	lence R.; Za 3-327: immun immun	(man)		126 129 124	108 F01	108	129 111	125	108	108	132	125	108	
	atic	Zachau, Zachau, 271, 199 munoglob MUID:94			NNN	H 6	, –	– 2	N	,	→ 6	N	N	_	
Score 483; DB 2; Pred. No. 1.1e-32; 7; Mismatches 5	,ACCESSION: \$40331 ,Status: preliminary; translation not shown ,Status: preliminary; ,Molecule type: mRNA ,Molecule type: mRNA ,Residues: 1-123 <klb> ,Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; ,Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; ,Superfamily: immunoglobulin V region; immunoglobulin homology ,Keywords: heterotetramer; immunoglobulin ,32-106/Domain: immunoglobulin homology <imm></imm></klb>	on 26-May-1999 H.G. lin chi genes 80891; PMID:8		ALIGNMENTS	\$40335 \$40369 \$40336	KIHUGL S31978	KVMS54	S52789 KVMS84	S40349	KIHUBN	KIHIDAII	S38646	S40350	KIHUKA	
2; Length 123; 32; 5; Indels 4; Gaps 1;	PIDN:CAA51109.1; PID:g441351 globulin homology	5 #text_change 21-Jan-2000 and their hypermutation.				kappa chain	kappa chain V	Ig kappa chain V r Ig kappa chain V r	kappa chain v-	kappa chain	Ig kappa chain V-I	kappa chain V	kappa	Ig kappa chain V-I	

RESULT 2 \$40367 Ig kappa chain V-J-C region - human C; species: Homo sapiens (man) C; Accession: \$40367 R; Klein, R.; Jaenichen, R.; Zachau, H.G. Bur. J. Immunol. 23, 3248-3271, 1993 A; Title: Expressed human immunoglobulin chi genes and their hypermutation. A; Reference number: \$40312; MUID: 94080891; PMID: 8258341 A; A; Accession: \$40367 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;33-107/Domain: immunoglobulin homology <IMM> A;Status: preliminary; translation A;Molecule type: mRNA A;Residues: 1-127 <KLB> 밁 S 밁 δ A; Cross-references: EMBL: X72477 Query Match 61 17 73 -GVPSRPSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIK 111 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTERTFGQGTKVEIK 123 DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLBS DIQMTQSPSSLSASVGDRVTITCRASQSIS---Score 482; not shown DB -sylnwyqqkpgkapklliyaasslqs 2 Length 127; 60 72

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RESULT 3
B49047
B49047
II (monoclonal striational autoantibody StrAB SA-IA) - human (fragm C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C; Accession: B49047
R; Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Bur. J. Immunol. 22, 2231-2236, 1992
A; Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A; Reference number: A49047; MUID:92387224; PMID:1516616
A; Accession: B49047
  Ś
                                                                                                                                                                                                                                                                                                                                                R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
S40370
                                              밁
                                                                                                                                                                                                                    C; Keywords: heter F; 30-104/Domain:
                                                                                                                                                                                                                                 A;Cross-references: EMBL:X72480; NID:g441428; PIDN:CAA51148.1; PID:g441429 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramez; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Experimental source: thymic B lymphocytes
A,Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunorlobulin homo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      닭
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                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-122 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Homo sapiens (man)
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                                                                                                                                l Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114
                                                                                    DIOMTOSPSSLSASVGDRVTITCRASOSVSTSSYSYMHWYQQXPGKAPKVLISYASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIQMTQSPSSLSASYGDRVTITCRASQSIS----NYLNWYQRKPGKAPKLLIYAASSLQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIOMTOSPSSLSASVGDRVTITCRASOSVSTSSYSYMHWYOOKPGKAPKVLISYASNLES
GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVPSRFSGSGSGTDFTLTISSLOPEDFATYYCQHSWGIPRTFGQGTKVEIKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIQMTQSPSSLSASVGDRVTITCRASQSIS----SYLNWYQQKPGKAPKLLIYAASSLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYNTPWTFGQGTKVEIKRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVEIKR 108
                                                                                                                                                                                                               immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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83.9%;
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                                                                                                                           Score 473; DB 2; Length 122; Pred. No. 7e-32; 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 474; DB 2; L
Pred. No. 5.2e-32;
"" matches 7;
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9; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 108
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C;Accession: S31998
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations
A;Reference number: S31977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin R;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P01600
A;Note: the C region of this chain has the Inv (3) marker
R;Steiner, V: Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances th.
A;Reference number: S02572; MUID:88005152; PMID:3115831
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R;Watanabe, S.; Hilschmann, N.
HOppe-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970
A;Title: The primary structure of a monoclonal kappa-type
A;Reference number: A01868; MUID:71032830; PMID:4097974
A;Accession: A01868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995
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C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: A01868; S02574
                                                                                                                                                                                    A,Cross-references: EMBL:Z15081; NID:g38501; PIDN:CAA78790.1; PID:g38502 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-109 < POR>
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                                                                                                                                                           F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                     A; Accession: S31998
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                                                                            Query Match
Best Local
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1 DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES 60
                                                                               Similarity
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                                             77.3%; Score 459; DB 2; 79.6%; Pred. No. 8.7e-31; tive 11; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 462; DB 1;
pred. No. 4.9e-31;
8; Mismatches 8
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Eur. J. immunol. 23, 3248-3271, 1993
A.Title: Expressed human immunoglobulin chi genes and their hypermutation.
A.Reference number: $40312; MUID:94080891; PMID:8258341
A.Accession: $40352
A.Status: preliminary; translation not shown
A.Status: preliminary; translation not shown
A.Residues: 1-131 < KLIS-
A.Residues: 1-131 < KLIS-
A.Residues: 1-131 < KLIS-
A.Residues: 1-131 < KLIS-
A.Cross-references: EMBL:X72462; NID:g441392; PIDN:CAA51130.1; PID:g441393
C.Superfamily: immunoglobulin vegion; immunoglobulin homology
C.Keyworda: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain V-J-C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change C;Accession: $40352 R;Klein, R.; Jaenichen, R.; Zachau, H.G. Eur. J. Immunol. 23, 3248-3271, 1993
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S40352
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A,Status; preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-108 <HAW>
A,Residues: 1-108 <HAW>
A,Cross-references: EMBL:Z31390; NID:g472976; PIDN:CAA83265.1;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                 GVPSRFSGSGSGTDFTLTISSLQPEDPATTYYCQHSWGIPRTFGQGTKVEIKRTV 114
                                                                                                                                            DIQMTQSPSSLSASVGNRVTITCRASQGIS----NYLAWYQQKPGKVPKLLIYAASTLQS
                                                                                                                                                                                            DIOMTOSPSSLSASVGDRVTITCRASOSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
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                                                               GVPSRFSGSGSGTDFSLTISSLQPEDVATYYCQKYNSVPRTFGQGTKVEIKRTV
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79.8%;
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Pred. No. 1.5e-30;
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K;FOTTOIANO, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations A;Reference number: S31977
A;Accession: S31981
Ig kappa chain - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (C)Species: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change C;Accession: $40317 R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hype A;Reference number: $40312; MUID:94080891; PMID:8258341
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IS Abpachain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31981
R;Portclano, S; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapopo.
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R;Reininger, L: Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, Bur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse A;Reference number: S09955; MUID:90269328; PMID:2347362
A;Accession: S09963
A;Molecule type: mRNA
A;Residues: 1-111 <REI>A;Residues: 1-111 <REI
A;Residues: 1-111 <REI
A;R
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C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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78.8%;
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74.8%; Pred. No. 2.7e-30;
tive 14; Mismatches 14
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Pred. No. 1.8e-30;
9; Mismatches 11
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Ig kappa chain C; Species: Homo C; Date: 06-Jan-C; Accession: S4
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A; Nolecule type: mRNA
A; Residues: 1-108 <MCI>
A; Residues: 1-108 <MCI>
A; Residues: references: EMBL:X79786; NID:g506422; PIDN:CAA56182.1; PID:g506423
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 16-90/Domain: immunoglobulin homology <IMM>
                                                         Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40333
A;Status: preliminary; translation not shown
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P. submitted to the EMBL Data Library, June 1994

A;Description: Cloning and analysis of IgM anti-thyroglobulin A;Reference number: S47181
                                                                                                                                                                                                                                                               RESULT 13
S40333
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A;Molecule type: mRNA
A;Residues: 1-129 <KLE>
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Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change;
Accession: S47182
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                                          immunoglobulin
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78.6%;
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80.2%;
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Pred. No. 3.9e-30;
.2; Mismatches 8
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Pred. No. 3.1e-30;
8; Mismatches 10
  Score 448;
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Length 125;
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GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIK

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A;Molecule type: mRNA
A;Residues: 1-106 <ESP>
A;Cross-references: EMBL:X75387
C;Superfamily: immunoglobulin V region; immunoglobu
C;Superfamily: immunoglobulin homology <IMM's
F;16-90/Domain: immunoglobulin homology <IMM's
F;24-34/Region: complementarity determining region
F;50-56/Region: complementarity determining region
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A; Title: Phage display of a human antibody
A; Reference number: PC2397; MUID:95011651;
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                                                                                                                                                                   A;Cross-references: EMBL:X72424
C;Superfamily: immunoglobulin V region; imm
C;Keywords: heterotetramer; immunoglobulin
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Eur. J. Immunol. 23, 3248-3271, 1993
A;Tille: Expressed human immunoglobulin chi genes and their
A;Reference number: S40312; MUID:94080891; PMID:8258341
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C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995
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닭
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                                                                                                                                                                                                                                                                                                                                                                           C; Accession: S40314
                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 06-Mar_1994 #sequence_revision 26-May-1995
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Best Local (
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DIQMTQSPSSLSASVGDRVTITCRASQSIN----NYLNWYHQKPGKAPNLLISAASSLQS
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81.1%;
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Pred. No. 7.3e-30;
8; Mismatches 8;
                                                                         Pred. No. 9.2
9; Mismatches
                                                                                           Score 447; DB 2;
Pred. No. 9.2e-30;
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B; Mismatches 9;
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Db 72 GVPSRFSGSGSGTDFTLIISSLQPEDFGTYYCQQTHTTPPTFGQGTKVEIK 122

Search completed: December 29, 2004, 19:36:34 Job time : 24.9742 secs

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Maximum Match 100%
Listing first 45 summaries
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1: uniprot_sprot:*
2: uniprot_trembl:*
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   DIQMTQSPSSLSASVGDRVT.....SWGIPRTFGQGTKVEIKRTV
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KV1A_HUMAN
KV1O_HUMAN
Q920E9
Q72473
KV3S_MOUSE
Q6GMX9
KV1P_HUMAN
KV1S_HUMAN
KV1Y_HUMAN
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Q6PIT5
AAH29444
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KV1E HUMAN
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KVLN HUMAN
KV1W HUMAN
KV1W HUMAN
KV1B HUMAN
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                                                                                  O9ul77 homo sapien P01600 homo sapien O5gmx8 homo sapien O5gmx9 homo sapien O5gmx0 homo sapien O5gmx0 homo sapien O5gmx1 homo sapien O5gl47 homo sapien O9ul70 homo sapien P01606 homo sapien P01431 homo sapien P01603 homo sapien P01603 homo sapien P0160430 homo sapien P01674 mus musculu P01674 mus musculu P01599 homo sapien O6glt5 homo sapien O6glt69 mus musculu O7z473 homo sapien O92009 mus musculu
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Best Local S
Matches 92
 -KV1H HUMAN
P01600;
21-JUL-1986
21-JUL-1986
01-OCT-2004
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SEQUENCE
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Q9UL77;
01-MAY-2000
01-MAY-2000
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69.2	69.2	69. 5	70.2	70.4	70.5	70.5	70.9	71.0	71.1	71.5	71.5	71.5
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AAH17870	Q6PJB5	KV1L HUMAN	KV3U_MOUSE	KV1R_HUMAN	AAH34146	Q6PIH4	KV1C_HUMAN	KV1D_HUMAN	KV1T_HUMAN	Q9UL79	KV1M_HUMAN	KV1F_HUMAN
70 ho	Q6pjb5 homo sapien	P01604 nomo sapien P01672 mus musculu	P01673 mus musculu	P01610 homo sapien	Aah34146 homo sapi	Q6pih4 homo mapien	P01595 homo sapien	P01596 homo sapien	P01612 homo sapien	Q9ul79 homo sapien	P01605 homo sapien	P01598 homo sapien

ALIGNMENTS

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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035037; AAD56273.1; -.
PIR; B49047; B49047.
PIR; B34083; S34083.
HSSP; P01607; 1BWW.
InterPro; IPR007;110; Ig-11ke.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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MEDLINE=99277139; PubMed=9614934;

Mu X., Liu B., Van der Merwe P.L.,

Young D.C.;
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01.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
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fetus.";
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92; Conservat
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                                                                                                                   GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIKR 108
                                                                                                                                              GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKR
                                                                                                                                                                                                         DIQMTQSPSSLSASVGDRVTITCRASQSIS----SYLNWYQQKPGKAPNLLIYAASSLQS
                                                                                                                                                                                                                                                                                                                                                                                                 108 AA;
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STANDARD;
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11738 MW; C06681716C4D16F3 CRC64;
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108
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RESULT QGMX8
ID Q6
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TISSUE=Primary B-Cells;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

Klausher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., High F.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hang J., Hsieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Niatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Niatchenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The primary s
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3D-structure; Bence-Jones pr.
Immunoglobulin V region
DOMAIN
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05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SMART; SM00406; IGv;
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-!- MISCELLANEOUS: The C re-
-!- MISCELLANEOUS: This is
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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InterPro; IPR003596; Ig_v.
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MEDLINE=71032830;
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GO:0005576; C:extracellular; N/
GO:0003823; F:antigen binding;
GO:0006955; P:immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57
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4 (TrEMBLrel.
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82.1%;
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ence-Jones Protein Hau): subdivision within
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Last sequence up
Last annotation
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Pred. No. 2.7e
8; Mismatches
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No. 2.7e-37;
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Best Local (
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InterPro; IPR00710; Ig-like.
InterPro; IPR00710; Ig-like.
InterPro; IPR003597; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00654; Cl-set; I.
Pfam; PP00047; Ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96SA9;
Q96SA9;
01-DEC-2001
01-DEC-2001
01-MAR-2004
  PIR;
PIR;
                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=98375893; PubMed=9712075;

Adderson E.F., Shikhman A.R., Ward K.B., Cunningham "Molecular analysis of polyreactive monoclonal antib rheumatic carditis human anti-N-acetylglucosamine/a
                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; F
Pfam; F
SMART;
SMART;
SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Primary B-Cells;
Strausberg R.;
Submitted (JUN-2004) to the
EMBL; BC073764; AAH73764.1;
                                                                  rheumatic carditis human anti-
antibody V region genes.",
J. Immunol. 161:2020-2031(1998)
EMBL, U96396, AAB68785.1; -.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                  variable
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"Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
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B49047;
PH0867;
S16840;
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236 AA, 2
PH0867.
S16840.
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                                                                                                                                                                                                                                                                                                                                                                   (Human)
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Primates;
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                                                                                                                                               anti-N-acetylglucosamine/anti-myosin
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Pred. No. :
                                                                                                                                                                                                                                                                                                                       Craniata; Vo
Catarrhini;
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Strausberg R;
Strausberg R;
Submitted (JUN-2004) to the EMBL
Submitted (JUN-2004) to the EMBL
EMBL; BC073775; AAH73775.1; -.

InterPro; IPR003599; Ig.
InterPro; IPR003199; Ig.
InterPro; IPR003199; Ig.
InterPro; IPR003199; Ig.
InterPro; IPR003199; Ig.
INTERPO; IPR003199; Ig.
INTERPO; IPR0031996; Ig.
INTERPO; IPR0031996; Ig.
INTERPO; IPR0031996; Ig.
INTERPOS; IPR0031996; Ig.
INTERPOS; 
                                                                                                                                                                                                                                                                                                                                                                                                           CTISSUE-Spleen; N.A.

X MEDLINE-Spleen; PubMed=12477932;
X MEDLINE-Spleen; P.L., Feingold E.A., Grouse L.H., Derge J.G.,
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
X Klausner R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,
X Klausner R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
X Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
X Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hong L.,
X Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hong L.,
X Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,
X Hopkins R.F., Jordan R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
X Hopkins R.F., Vodus M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
X Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
X Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
X Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
X Barownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
X Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
X Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Willalon D.K., Muzny D.M., Sodergren B.J., Dickson M.C.,
X William M., Touchman J.W., Green B.D., Dickson M.C.,
X Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
X Hones S.J., Marra M.A.,
X Jones S.J., Marra M.A.,
X Jones S.J., Marra M.A.,
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PIR; 834083; 834083.

PIR; 834086; 834086.

HSSP; P01607; 1BWW.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

Pfam; PP00047; 19; 1.

SMART; SM00406; IGV; 1.

PROSITE; P850835; IG_LIKE; 1.
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                           Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
Generation and initial analysis of more than 15,000
"Generation and initial analysis of more than 15,000
more CNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKR
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11520 MW;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 456.5; DB 2
Pred. No. 9.1e-37;
7; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4BB43E9C5B577F16
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RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max R.N., Rubin G.M., Hong L.,

RA Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Bitchenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Bitchenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Bitchenko L., Modrigues M.B., Bonaldo M.F., Casavant T.L., Scheez T.,

Ra Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Willialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

William M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,

Ra Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,

Ra Krzywinski M. I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,
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Best Local Similarity
                 Strausberg R.;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073791; AAH73791.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003199; Ig.-like.
InterPro; IPR003597; Ig.-c1.
InterPro; IPR003086; Ig.MHC.
InterPro; IPR003086; Ig.MHC.
InterPro; IPR003086; Ig.MHC.
InterPro; IPR003597; Ig.-c1.
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Q6GMW1;
05-JUL-2004
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05-JUL-2004
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SMART; SM00409; IG; 2.

SMART; SM00407; IGC1; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 2.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 Pfam;
Pfam;
SMART;
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TISSUE=Spleen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
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SEQUENCE 23
InterPro; IPR003596; IQPfam; PF07654; C1-set; Pfam; PF00047; 1g; 2. SMART; SM00409; IG; 2.
                                                                                                                                                                                                                                                                                                                 Jones S.J., Marra M.A.;
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                                                                                                                                                                                                                                                         on and initial analysis of cDNA sequences.";
1. Acad. Sci. U.S.A. 99:168
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236 AA; 2
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78.1%;
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Last annotation update)
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Pred. No. 3.1e-36;
2; Mismatches 9;
                                                                                                                                                                                                                                                               99:16899-16903 (2002)
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Catarrhini; Hominidae;
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XS trausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XA Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,

XA Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,

XA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XA Diatchenko L., Marusina K.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XA Stapleton M., Usdin T.B., Toshiyuki S., Carringon R.D., Mullahy S.J.,

XA Barowstein M.J., Usdin T.B., Toshiyuki S., Carringon R.D., Mullahy S.J.,

XA Barowstein M.J., McKernan K.J., Malek J.A., Gibbs R.A.,

XA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XA Wilting M., Wadan A., Young A.C., Shevchenko Y., Butterfield Y.S.,

XA Krywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

XA Jones S. J. Marra M. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                     InterPro; IPR003599; Ig.
InterPro; IPR003199; Ig-like.
InterPro; IPR003197; Ig-like.
InterPro; IPR003197; Ig-d1.
InterPro; IPR003196; Ig-MHC.
InterPro; IPR003196; Ig-MHC.
InterPro; IPR003196; Ig-V.
Pfam; PF07654; C1-Bet; I.
Pfam; PF07654; C1-Bet; I.
SMART; SM00407; Ig-2.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS00220; IG_MIC; UNKNOWN.
Hypothetical protein.
SEQUENCE 236 AA; 25751 MW; 5BI
                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (JUL-2002) to the EM Submitted (JUL-2002) to the EM EMBL; BC034141; AAH34141.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q6PIH7;
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6PIH7
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                                                                                                                                                                                                                                                                                                                                                                                                             rissum=Lung;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neration and initial analysis of more than 15,000 full-length mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SC1.
   IG_LIKE;
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80.5%;
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27,
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Last sequence update)
Last annotation updat
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Pred. No. 3.9e-36;
6; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RA Strausberg R.D., Cellins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.E., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.E., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heleh F., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., RA Stapleton M., J., Walki S., Carninci P., Prange C., RA Stapleton M., Koquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.J., J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Moriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Karywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E., Karywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
                                                                                                                                                                                                               Query Match
Best Local S
Matches 90
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02-MAR-2004
02-MAR-2004
02-MAR-2004
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Hypothetical protein.

SEQUENCE 236 AA; 25603 MW; 8BC56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 236 AA; 2
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2002) to the EMBL; BC034141; AAH34141.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    fissuE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.; Generation and initial analysis of more than 15,000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
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                                                                                                          23
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                                                                                                                                                                                                                                          Similarity
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DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
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Primates;
                                                                                                                                                                                                                                          74.7%;
78.9%;
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78.9%;
                                                                                                                                                                                                                                                                                                                         25603 MW;
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Last
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Pred. No. 3.
                                                                                                                                                                                                                                          Score 444; DB 2;
Pred. No. 3.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99:16899-16903 (2002)
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annotation update)
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.7e-35;
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                                                                                                                                                                                                                                                                  236;
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J.E.,
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Best Local &
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21-JUL-1986 (Rel. 0:
05-JUL-2004 (Rel. 4:
Ig kappa chain V-I :
MEDLINE-98277139; PubMed-9614934; MEDLINE-98277139; PubMed-9614934; "1" B. Van der Merwe P.L.
                                                                                                                                            Q9UL70;
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01-MAY-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NA GO; GO:0006955; P:immune response; NA InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                              (Fragment).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - MISCELLANEOUS:
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                                                                                                                                                                                                                                                             DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
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EMBLrel. 13, Last sequence update)
EMBLrel. 25, Last annotation update)
immunoglobulin light chain variable
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                                                          Chordata;
Primates;
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77.7%;
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                                                                                                                                                                                                                                                                                         Score 441; DB 1
Pred. No. 3e-35;
9; Mismatches
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                                                          Craniata; Vo
Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                         similarity.
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                                                                   Vertebrata; Euteleostomi;
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                                                          Hominidae;
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P01606;
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"Myosin-reactive autoantibodies
fetus.";
Clin. Immunol. Immunopathol. 87:
                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                       MEDLINE=70201507; PubMed=5447531;
Kohler H., Shimizu A., Paul C., P
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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SMART; SM00406; IGv;
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                                                                                                                                                                                                                             Science 169:56-59(1970)
                                                                                                                                                                                                                                      chains."
                                                                                                                                                                                                                                             "Macroglobulin structure: variable
                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                 kappa chain
                                                                                                                                                 P, P01607, 1BWW.
GG:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding; NAS.
GO:0006955; P:immune response; NAS.
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                n sequencing;
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G_LIKE;
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Ig_v.
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chain was isolated from a Waldenstrom's
WW;
               Framework-2.
Complementarity-determining-2.
Framework-3.
Complementarity-determining-3.
Framework-4.
By similarity.
                                                                                          Immunoglobulin
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Pred. No. 3e-3
5; Mismatches
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                                                                        Complementarity-determining-1.
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Catarrhini; Hominidae;
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8283D4A24105827E
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ble sequence
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RESULT 12
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SMART; SM00406; IGv; 1.
SMART; PS50835; IG LIKE;
PROSITE; PS50835; IG LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities required the statement are not removed. Usage by the for commercial
                                                                                                            DISULFID NON_TER
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                      entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=85014148; PubMed=6091049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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-UUL-1999 (Rel. 38, Last annotation update)
kappa chain V-I region Walker precursor.
                                                                                                                                                                                                                                                                                                                   GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding; NAS.
GO:0006955; P:immune response; NAS.
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                        ğ
DIQMTQSPSSLSASVGDRVTITCRASQSIS----NYLNWYQQKPGKAPKLLIYAASSLQS
               .QMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
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                                                        74.1%;
79.3%;
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Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.
Complementarity-determining-3.
Framework-4.
                                             Score 440; DB 1; 1
Pred. No. 4.6e-35;
0; Mismatches 9;
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Pred. No. 3.7e-35;
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RA Allausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Brownstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Brownstein M.J., Wackernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
RA Jones S. T. Mayrra M.A.,
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_wHC.
InterPro; IPR003596; Ig_w.
Pfam; PF07554; Cl-set; 1.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Skeletal Muscie;
Strausberg R.;
Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7Z3Y4;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                              Hypothetical SEQUENCE 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Skeletal Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                        Local
                                                          61
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   79
                                                                                                                                                                               \vdash
                                                                                                                                                                                                                                         ; 68
                                                                                                                                                                                                                                                                        Similarity
                                              GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114
                                                                                                                                                            DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIK 111
GVQSKFSGSGSGTDFTLTISSLQPEDFATYYCQQYKSYPVTFGQGTKLEIKRTV
                                                                                                                       DIQMTQSPSSLSASVGDTVTITCRASQDIS----NYLAWFQQKPGKAPKSLIYGASSLQS
                                                                                                                                                                                                                                                                                                                                                           al protein.
236 AA; 2
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(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                         Conservative
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Primates;
                                                                                                                                                                                                                                                                     74.1%;
78.1%;
                                                                                                                                                                                                                                                                                                                                                              25702 MW;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                  Score 440; ub .,
No. 9.1e-35;
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                              7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                                                                                                                                                                                                                                   236;
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RESULT 15
KV1B_HUMAN
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KV1K_HUMAN
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Best Local
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P01594;
21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
01-OCT-2004 (Rel. 45,
01-OCT-2004 (Rel. 45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, 05-JUL-2004 (Rel. 44, Ig kappa chain V-I re Homo sapiens (Human).
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P01603;
                                                                                                                                              RV1B
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NON_TER
SEQUENCE.
MEDLINE=72189444; PubMed=5028201;
Schiechl H., Hilschmann N.;
                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0005855; P:immune response; NAS. InterPro; IPR007110; Ig-11ke. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Comparative structural studies on the light chains of human immunoglobuling. I. Protein Ka with the Inv(3) allotypic marker.";
J. Blochem. 77:1277-1296(1975).
-I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-I- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Bence-Jones protein; Direct p
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv;
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HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                            no sapiens (Human)
                                                                                                                                                 HUMAN
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                                                                                                                                                                                                                                                                                            82;
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                                                                                                                                                                                                   GVPSRPSGQGSGTBFTFTISSVZPZBFATYYCQZYLDLPRTFGQGTKVDLKR
                                                                                                                                                                                                                 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVBIKR 112
                                                                                                                                                                                                                                                               DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
                                                                                                                                                                                                                                               QMTQSPSTLSVSVGDRVTITCEASQTV----LSYLNWYQQKPGKAPKLLIYAASSLET
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                                                                                                                                              STANDARD;
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01, Last
44, Last
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01, Last sequence update)
45, Last annotation update)
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73.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein sequencing;
                                                                                                                                                                                                                                                                                          Score 438; DB
Pred. No. 5.9e
L5; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Framework-3.
Complementarity-determining-3
Framework-4.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                      Complementarity-determining-2
                                                                                                                                                                                                                                                                                                                                                                                                                  Framework-2.
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                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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on update)
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Best Local S
Matches 88
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DOMAIN 24
DOMAIN 35
DOMAIN 57
DOMAIN 57
DOMAIN 57
DOMAIN 59
DOMAIN 98
DISULPID 23
STRAND 10
STRAND 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";
                                                                                                                                                                                                                                                                                                                                                                                                          8888
                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A91653; KIHUAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pehlhammer H., Schiffer M., Epp O., Schwager P., Steigemann W., Schramm The structure determination of the
                                                                                                  SEQUENCE
                                                                                                                                                                                            STRAND
                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG LIKE; 3D-structure; Bence-Jones [
                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406;
                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hoppe-Seyler's 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones protein Au."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=77022433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                        ; 1JV5; X-ray; A=1-107.
GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding; NAS.
GO:0006955; P:immune response; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecular replacement methods
region of the kappa chain REI.
MISCELLANEOUS: The C region of
MISCELLANEOUS: This is a Bence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phys. Struct. Mech. 1:139-146(1975).
MISCELLANEOUS: The structure of the V region version of the V region versions are replacement methods using the known
57
              61
                                                                 88;
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                                                 \vdash
                                                                         Similarity
              GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVBIKR
                                DIQMTQSPSSLSASVGDRVTITCQASQDIS----DYLNWYQQKPGKAPKLLIYDASNLES
                                                DIOMTOSPSSLSASVGDRVTITCRASOSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
ĠVPŚŔFŚĠĠĠĠĠAHFTFT
                                                                 Conservative
                                                                                                                                                   7665554430774
                                                                                                  A,
                                                                                                                                                                                                                                                                                                                                              V region.
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                                                                                                                 73.6%;
78.6%;
                                                                                                  11939 MW;
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                                                                                                                                                                                                                                                                                                                                                        protein;
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                                                                6
                                                                       Score 437; DB 1;
Pred. No. 7.3e-35;
                                                                                                                                                                                                                                                                                      Complementarity-determining-3. Framework-4.
                                                                                                                                                                                                                                                                                                       Complementarity-determining-2. Framework-3.
                                                                                                                                                                                                                                                                                                                      Framework-1.
Complementarity-determining-1.
Framework-2.
                                                                                                                                                                                                                                                                              By similarity
                                                                                                  E8011187EE6F6FB9 CRC64;
                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                        Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colman P. H.J.; variable
ATYYCQQYDYLPWTFGQGTKVBIKR
                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.M., Lattman
                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            portion
                                                                                Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                        sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure
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108
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Job time : 128.21 secs

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB seq length: 0
DB seq length: 2000000000
                                                                                                                                                                                                                                                                                   Score
        US-10-044-896-3
594
      100.
83.20.
82.35.
82.35.
82.36.
81.88.
81.88.
81.88.
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                                                                                                                                                                                                                                                                                     Match
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                                                                                                                                                                                                                                                                                                         Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      December 29, 2004, 19:36:01; Search time 93.9399 Seconds (without alignments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA:*
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : /cgn2 6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
: /cgn2 6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
: /cgn2 6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
: /cgn2 6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
: /cgn2 6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
: /cgn2 6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
: /cgn2 6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /cgn2 6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /cgn2 6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
: /cgn2 6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
: /cgn2 6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
: /cgn2 6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
: /cgn2 6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
  14 US-10-044-896-3
15 US-10-378-567-3
9 US-09-917-410-2
14 US-10-216-484-127
14 US-10-384-933-127
14 US-10-384-933-131
14 US-10-384-933-131
19 US-09-920-171-10
10 US-10-384-933-131
19 US-09-920-177-9
9 US-09-920-077-9
9 US-09-802-096-9
9 US-09-920-171-13
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Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 127, App
Sequence 127, App
Sequence 131, App
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appli
Sequence 9, Appli
                                                                                                                                                                                                                                                                                 Description
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ALIGNMENTS

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APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Jin K.
APPLICANT: Kim, Jin K.
APPLICANT: Stewart, Timothy
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
FILE REFERENCE: GENENT.074A
CURRENT APPLICATION NUMBER: US/10/044,896
CURRENT FILING DATE: 2002-01-09
FRIOR APPLICATION NUMBER: 60/270775
PRIOR APPLICATION NUMBER: 60/270775
PRIOR APPLICATION NUMBER: 60/270775
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 114
TYPE: PRT
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                                                                                                                                                                                                                                                                                       US-10-044-896-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10044896
Publication No. US20030166228A1
                                                                                                                                                                               Query Match 100.0%; Score 594; DB 14; Best Local Similarity 100.0%; Pred. No. 1.8e-40; Matches 114; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: This sequence represents a humanized chimeric OTHER INFORMATION: antibody comprising human and non-human sequences.
61 GVPSRFSGSGGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114
                                                                          DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
                                                                                                                                                                               Indels 0;
                                                                                                                                                                                                                               Length 114;
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GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114

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RESULT 3
US-09-917-410-2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/378,567
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: PCT/US01/27352
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 60/276,452
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TAYLOR, FREDERICK R.
APPLICANT: ZHENG, ZHONGLI
TITLE OF INVENTION: CO-CRYSTAL STRUCTURE OF MONOCLONAL ANTIBODY 5C8 AND
TITLE OF INVENTION: CD154, AND USE THEREOF IN DRUG DESIGN
FILE REFERENCE: A096CON1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/229,933
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KARPUSAS, APPLICANT: HSU, YEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 218
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: humanized 5c8 light chain amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII, WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MARTIN, Ulrich; HASBLBECK, Anton; SCHUMACHER, Guenther; CO, Man S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVLTQSPATLSVSPGERATISCRASQRVSSSTYSYMHWYQQKPGQPPKLLIKYASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                     STATE: New York
APPLICATION NUMBER: US/09/917,410
                                                                                                                                                                              COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                       ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                          T: 805 Third Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEN-MING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.2%; Score 494; DB 15; 79.8%; Pred. No. 3.7e-32; tive 13; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                        EXTRACORPOREAL BLOOD CIRCULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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; OTHER INFORMATION: Description of Artificial Sequence: Designed light; OTHER INFORMATION: chain of humanized anti-Fas antibody US-10-216-484-127
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                                     S
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT APPLICATION NUMBER: US/99/499,662
PRIOR APPLICATION NUMBER: US/99/499,662
PRIOR APPLICATION NUMBER: US/99/499,662
PRIOR FILING DATE: 2000-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
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                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 165
SEQ ID NO 127
                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/053,583 PRIOR FILING DATE: 1998-04-01
                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 838-31
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 26-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMER: 08/578,953
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020098183Alman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GIPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPWTFGQGTKVEIKRTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
                            DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES
DIVLTOSPSSLSASVGDRVTITCKASOSVDYDGDSYMWYQQKPGKAPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIQMTQSPSSLSASVGDRVTITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10216484 o. US20030103976A1
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                                                                                                    82.3%;
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                                                                                                Score 489; DB 1
Pred. No. 1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 490; DB 9;
Pred. No. 7.8e-32;
                                                                                                                      DB 14;
                                                                                   12;
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                                                                                                                      Length 238;
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GVPSRFSGSGSGTDFTLTISSLQPEDFATTYCQHSWGIPRTFGQGTKVEIKRTV 114

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APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Hideyuki
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OP INVENTION: Anti-Pas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-03,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 131
, OTHER INFORMATION: Description of Artificial Sequence: Designed light , OTHER INFORMATION: chain of humanized anti-Fas antibody US-10-216-484-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-216-484-131
; Sequence 131, Application US/10216484
; Publication No. US20030103976A1
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US-10-384-933-127
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SEQ ID NO 127
LENGTH: 238
TYPE: PRT
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Publication No. US20030170817A1
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TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT FILING DATE: 2003-02-05
FRIOR APPLICATION NUMBER: US/99/499,662
PRIOR PILING DATE: 2000-02-09
PRIOR PILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
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APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
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                                                                        ORGANISM: Artificial Sequence FEATURE:
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Nakahara, Kaori
Tamaki, Ikuko
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86.0%;
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Pred. No. 1e-31;
4; Mismatches 12;
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                                                                                                                                                                                                                                                                            Sequence 10, Application US/09920171 Patent No. US20020054878A1 GENERAL INFORMATION:
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SEQ ID NO 131
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Best Local Similarity
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                                                           TITLE OF INVENTION: Improved Anti-IgE Antibodies FILE REFERENCE: P1123C2US CURRENT APPLICATION NUMBER: US/09/920,171 CURRENT FILING DATE: 2001-08-01 PRIOR APPLICATION NUMBER: US 08/887,352 PRIOR FILING DATE: 1997-07-02
                                                                                                                                                                                         APPLICANT: Lowman, Henry B.
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
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PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
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CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
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TITLE OF INVENTION: Anti-Fas Antibodies
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APPLICANT: Haruyama, Hideyuki
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TYPE: PAT
TYPE: ORGANISM: Artificial Sequence
PEATURE:
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Tamaki, Ikuko
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85.1%;
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Pred. No. 1.2e-31;
5; Mismatches 12
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Pred. No. 1.2e-31;
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TITLE OF INVENTION: Improved Anti-IgB Antibodies
FILE REFERENCE: p11233US
CURRENT APPLICATION NUMBER: US/10/113,996
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR APPLICATION NUMBER: US 09/296,171
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
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; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Light chain sequence derived US-10-113-996-10
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        Sequence 10, Application US/10791619
Publication No. US20040259077A1
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P11281
CURRENT APPLICATION NUMBER: US/10/791,619
CURRENT FILING DATE: 2004-03-02
CURRENT FILING DATE: 2004-03-02
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SEQ ID NO 10
LENGTH: 114
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LENGTH: 114
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Best Local S
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PRIOR APPLICATION NUMBER: US/09/109,207
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Lowe, John
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No. US20030149244A1
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Pred. No. 8.8e-32
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Pred. No. 8.8e-32;
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APPLICANT: Dardieu, Paula M.
APPLICANT: Presta, Leonard G.
INTILE OF INVENTION: Method of Treating Allergic Disorders (as FILE REFERENCE: P0718F2C3US
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-07
PRIOR PILING DATE: 1992-05-07
PRIOR PILING DATE: 1992-08-14
PRIOR PILING DATE: 1991-08-14
RESULT 12
US-09-802-096-9
; Sequence 9, Application US/09802096
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US-09-802-077-9
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LENGTH: 114
TYPE: PRT
ORGANISM: Artificial
FEATURE:
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Best Local 8
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SEQ ID NO 9
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LOCATION: 1-114
OTHER INFORMATION: Light chain sequence derived
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                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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86.0%; Pred. No. 1.6e-31;
live 3; Mismatches 13
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Pred. No. 8.8e-32;
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61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHSWGIPRTFGQGTKVEIKRTV

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PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 13
LENGTH: 218
TYPE: PRT
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CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR PILING DATE: 1992-05-07
PRIOR PILING DATE: 1991-08-14
NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER: OF SEQ ID NOS: 64
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                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09920171
Patent No. US20020054878A1
GENERAL INFORMATION:
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                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended) FILE REFERENCE: P1123C2US CURRENT APPLICATION NUMBER: US/09/920,171 CURRENT FILING DATE: 2001-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lowman, Henry B. APPLICANT: Presta, Leonard
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                      OTHER INFORMATION: Light chain sequence derived from MAE11
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ITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders
ILB REFERENCE: P0718P2C3US
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les 98; Conservation
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                                           DIQMTQSPSSLSASVGDRVTITCRASQSVSTSSYSYMHWYQQKPGKAPKVLISYASNLES 60
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Jardieu, Paula M.
QLTQSPSSLSASVGDRVTITCRASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASYLES
                                                                                          Conservative
                                                                                                             81.8%;
                                                                                        3; Mismatches
                                                                                                           Score 486; DB 9;
Pred. No. 1.6e-31;
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Pred. No. 1.6e-31;
3; Mismatches 13
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PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 9
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PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 09/920,171
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
NUMBER: OF SEQ ID NOS: 44
                                                                                                                                                            TITLE OF INVENTION: Improved Anti-IgE Antibodies FILE REFERENCE: F1123C3US CURRENT APPLICATION NUMBER: US/10/113,996 CURRENT FILING DATE: 2002-04-01
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TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
FILE REFERENCE: P0718P2C1D1C1US
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APPLICANT: Presta, Leonard
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FILLING DATE: 1994-01-26
APPLICATION NUMBER: PCT/US92/06860
FILLING DATE: 1992-08-14
APPLICATION NUMBER: US 07/879,495
FILLING DATE: 1992-05-07
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Lowe, John
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86.0%;
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Pred. No. 1.6e-31;
3; Mismatches 13;
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Gapop 10.0 , Gapext 0.5
UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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                                                                                                                                                                                                                                                                                                                                                             US-10-044-896-5
634
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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.; A. 99:16899-16903(2002). le EMBL/GenBank/DDBJ databas .; ke iC. UNKNOWN_2.	RY SEQUENCE FROM N.A. RC TISSUE-Primary B-Cells; RC TISSUE-Primary B-Cells; RX MEDLINE-22388257; PubMed=12477932; RX MEDLINE-22388257; PubMed=12477932; RX MEDLINE-22388257; PubMed=12477932; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schule RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh RA Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L. RA Diatchenko L., Marusha K., Foshiyuki S., Carninci P., Pran RA Eloardein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pran RA Eloardein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pran RA Raha S.S., Loquellano N.A., Peters G.J., Abramaon R.D., Mull RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratn RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hu RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A. RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G. RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterf RA Generation and initial analysis of more than 15,000 full-le	ALIGNMENTS PRT; 470 AA. Created) Last sequence update) Last annotation update) Last annotation definition and the sequence	CAB45931 BAD00448 BAD00564 Q6FeC4 AAH62335 Q9UL93 BAD00471 AAL35875 BAD00487 BAD00487 BAD004893 BAD00564 BAD00564 BAD00566
	J.G., f., Schuler G.D., f., Heieh R.K., f., Hong L., hong L., p., prange C., c.D., Mullahy S.J., Gunaratne P.H., f.J., Hulyk S.W., libbs R.A., libbs R.A., scheard G.G., M.C., butterfield Y.S., shuterfield Y.S., butterfield J.E., full-length human	Euteleostomi,	Cae45931 homo sapi Bad00448 camelus d Bad00564 camelus d Q6p6c4 homo sapien Aah62335 homo sapien Bad00470 camelus d Bad00471 camelus d Aal35875 lama glam Bad00487 camelus d Bad00493 camelus d Bad00594 camelus d Bad00594 camelus d

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XX MEDLINE-22388257; pubMede1124777932;

XX MILESCHUL S.F., Feingold E.A., Grouse L.H., Derge J.G.,

XX Malusner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

XX Altschul S.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Brownstein M.J., Wedin N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XX Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Willalon D.K., Maton A., Young A.C., Shevchenko Y., Bouffard G.G.,

XX Hilalon D.K., Touchman J.W., Green E.D., Dickson M.C.,

XX Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

XX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Sutterfield Y.S.,

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02-MAR-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                   TISSUE=Primary B-Cells;
Strausberg R.;
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Mammalia; Eutheria;
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                                                                                                                                                                                                   Hypothetical protein. SEQUENCE 470 AA; 51715 MW;
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EVQLVESGGGLVQPGGSLRLSCVVSGFTFSSYMMSWVRQAPGKGLEWVANIKQDGSBKYY
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Best Local (
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01-MAY-2000
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02-MAR-2004
02-MAR-2004
                       fetus.";
Clin. Im
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma3 in vivo repertoires." Submitted (SEP-2002) to the EMBL; AB092163; BAD00525.1;
                                                                                                                    SEQUENCE FROM N.A. MEDLINE=98277139; I
                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                        Young D.C.;
"Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Libraries of heavy-chain antibodies reflecting camel gamma2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Spleen;
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                                                                                                                                                                                                                                                                                                                      (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 S 119
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  AF035024;
                            Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYC--ASWISDFFDYWGQGTLVTVSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
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121 AA;
                                                                                                                                                                                                                                                                                                                                               (TERMBLrel. 13, Created)
(TERMBLrel. 13, Last sequence update)
(TERMBLrel. 26, Last annotation updat
ive immunoglobulin heavy chain variab
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLel. 27, Last annotation update)
Lin heavy chain VHDJ region (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                            Immunopathol.
     AAD56260.1;
                                                                                                                         PubMed=9614934;
n der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12951 MW;
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71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Dromedary) (Arabian camel).
Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Tylopoda; Camelidae; Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurosawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                            87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 433.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>۲</u>
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                                                                          rheumatic carditis
                                                                                                                         Kalis
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                                                                                                                         N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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variable
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                                                                             and
                                                                                                                              S.M.
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RESULT 5
BADOG AC BADO
AC BADO
AC BADO
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DT 02-N
DT 02-N
DT 102-N
DT 102
       RESULT 6
Q6MZV7
ID Q6MZ
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Best Local S
Matches 83
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Best Local S
Matches 86
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
QGMZV7;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
4. Aporthetical protein DKFZp686C11235.
Name=DKFZp686C11235;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAD00414;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Honda T., Akahori Y., Kurosawa Y.;
"Libraries of heavy-chain antibodies
gamma3 in vivo repertoires.";
Submitted (SEP-2002) to the EMBL/GenE
EMBL; AB092052; BAD00414.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
1mmunoglobulin heavy chain VHDJ region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Spleen;
Honda T., Akahori Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                               DSVKGRFTISRDNAKOTLYLOMNSLKSGDTALYYCATSSSNSVDYWGQGTQVTVSSES
                                                                                                                                                                                                                                                                                                                                         QRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCASWISDFFDYWGQGTLVTVSSAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDL----NYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
120 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.5%;
nilarity 70.3%;
Conservative 11
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nilarity 73.5%;
Conservative
                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
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12724 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12437 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Dromedary) (Arabian camel). Chordata; Craniata; Vertebra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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Pred. No. 1.7e-
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 428; DB Pred. No. 1.8e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reflecting camel gamma2
                                                                                                                                                                                             473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
.7e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 113;
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         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
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CAB450
ID CAB4
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Best Loc
Matches
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Best Local Similarity
Matches 82; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Pobo G., Han M., Wiemann S.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

REMBL; BSK400853; CAS45920.1; -.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig_Gl.

R InterPro; IPR003597; Ig_Gl.

R InterPro; IPR003597; Ig_MHC.

R InterPro; IPR003596; Ig_MHC.

R InterPro; IPR003596; Ig_WC.

R InterPro; IPR003596; Ig_V.

R Pfam; PF07654; Cl-set; 3.

R Pfam; PF07054; Cl-set; 3.

R Pfam; PF00047; Ig; 4.

R PMART; SM00409; IG; 2.

R SMART; SM00409; IG; 2.

R SMART; SM00407; IGC1; 3.

R SMART; SM00406; IGV; 1.

R PROSITE; PS0083; IG_LIKE; 4.

R PROSITE; PS0083; IG_LIKE; 4.

R PROSITE; PS00090; IG_MHC; UNKNOWN 2.

SEQUENCE 473 AA; 52121 MW; 9476EAE4COBFC447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=Human small intestine;
THE GERMAN HUMAN CDNA CONSORTIUM;
Ploacker H., Boecher M., Mewes H.W.,
                                                                                                                                                                                                                                                                       TISSUE-Human small intestine;
Bloecker H., Boecher M., Mewes H.W., Weil B.,
Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ
EMBL; BX640853; CAE45920.1; -.
Hypothetical protein.
SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BFC44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAB45920;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686C11235.
DKFZP686C11235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAE45920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
[1]
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                                                                                                                                                                               Local
                                                                                                                                                                                                            Match
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                                                                                                                                                                        Similarity
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                                    EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
EIQLVESGGGLVQPGGSLRLSCAASGFTFSSFEMNWVRQAPGKGLEWLSYITRSGNTVYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIQLVESGGGLVQPGGSLRLSCAASGFTFSSFEMNWVRQAPGKGLEWLSYITRSGNTVYY
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                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Primata; C
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                                                                                                                                                                        67.4%;
65.1%;
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                                                                                                                                       13;
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                                                                                                                                       Score 427.5;
Pred. No. 9.8e
13; Mismatches
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Pred. No. 9.8e-37;
.3; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Craniata; \Catarrhini;
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                                                                                                                                                                                                                                                                                  9476EAE4C0BFC447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata;
; Hominidae;
                                                                                                                                                                           .8e-37;
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                                                                                                                                                                                                            DB
                                                                                                                                                                                                            2;
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                                                                                                                                                                                                                                                                                                                                                                                     databases
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                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                 Length
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                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osanger
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RESULT 9

BADOQ
AC BADO
DT 02-W
DT 02-W
DT 02-W
DT 02-W
DT Immu
GN IGVE
OC Euke
OC Mamma
OX NCBJ
RN [1]
RP SEQI
RC TISE
RA Honc
RT "Lill
RT Subr
DR EMBI
RT Subr
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BADDO40
ID BADO
AC BADO
AC BADO
AC BADO
DT 02--W
DT 103--W
DT 103-
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Best Local S
Matches 84
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02-MAR-2004
02-MAR-2004
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02-MAR-2004
02-MAR-2004
                                                                                                                                                                                                                                                                                                 BAD00444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAD00406;
TISSUE-Spleen;
Honda T., Akahori Y., Kurosawa Y.;
"Libraries of heavy-chain antibodies
gamma3 in vivo repertoires.";
Submitted (SEP-2002) to the EMBL/GenE
EMBL; AB092082; BAD00444.1; -.
NON_TER
                                                                                                                                          Euxaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9838;
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                                                                                                                                                                                                 Camelus dromedarius
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Mammalia, Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Camelus dromedarius
                                                                                                                SEQUENCE
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NCBI_TaxID=9838;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Honda T., Akahori Y., Kurosawa Y.;
"Libraries of heavy-chain antibodies
                                                                                                                                                                                                                              02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
03-MAR-2004 (TrEMBLrel. 27,
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02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
Immunoglobulin heavy chain V
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                                                                                                                FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADSLQGRFTISRDNARNSLYLQMNSLRAEDTAVYYCARQNEHTSPWYPSFFDYWGQGILV
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(SEP-2002) to the E
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13856 MW;
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                                                                                                                                                                                 (Dromedary) (Arabian camel). Chordata; Craniata; Vertebra
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Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Tylopoda; Camelidae; Camelus.
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Pred. No. 2.5e
14; Mismatches
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Last annotation update)
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Last annotation update)
                              EMBL/GenBank/DDBJ databases
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.5e-37;
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Q9UL71
Q9UL71;
01-MAY-2000
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                            ADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGKVTTIYDRFDIWGQGTMVTVS
                                                    NORFKGRETISLDKSKRTAYLQMNSLRAEDTAVYYCA----SWISDFFDYWGQGTLVTVS
                                                                                                     EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
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117
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121 AA;
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128 AA;
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13775 MW;
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Primates;
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                                                                                                                                               Score 426; DB 2
Pred. No. 3e-37;
9; Mismatches
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Pred. No. 2.5e-37;
2; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                           2F045CCFA5D50736 CRC64;
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Best Local &
Matches 82
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Best Local S
Matches 84
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02-MAR-2004
02-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                  gamma3 in vivo repertoires."
Submitted (SEP-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Spleen;
Honda T., Akahori Y., Kurosawa Y.;
"Libraries of heavy-chain antibodies reflecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
102-MAR-2004 (TrEMBLrel. 27, Last annotation update)
102-MAR-2006 (TrEMBLrel. 27, Last annotation)
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Submitted
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Mammalia; Eutheria;
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Submitted (SEP-2002) to the F
EMBL; AB092084; BAD00446.1;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Camelus dromedarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAD00520;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9838;
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onda T., Akahori Y.,
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NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCASWI---SDFFDYWGQGTLVTVSS
                                                                                               EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVQLVESGGGLVQPGGSLRLSCAASGFTFSNYYMTWVRQAPGKGLEWVSGINQDGSNTYY
                                                                       EVQLVESGGGLVQPGGSLRLSCAASGFTFSKFWMHWVRQAPGKGLEWVSGINPVGINTYY
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13526 MW;
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Chordata; Craniata; Vertebra
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chain VHDJ region (Fragment).
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                                                                                                                                                             Score 425.5; |
Pred. No. 3.4e
|4; Mismatches
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Pred. No. 3e-3
LO; Mismatches
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Scheefer C.F., Bhat N.K.,

RA Altschal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Farmer A.A., Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hulk S.J.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hilling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Holkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Goriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

RA Holland R. S., Schein J.E., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (APR-2001) to the
EMBL; BC006402; AAH06402.1;
Hypothetical protein.
SEQUENCE 479 AA; 52281 MV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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02-MAR-2004 (TrEMBLrel.
02-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones S.J., Marra M.A.; "Generation and initial analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52281 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.1%; Score 425.5; DB 2
65.2%; Pred. No. 1.6e-36;
bive 10; Mismatches 23
                                                                                                                                                                                                                                                    119
                                                                                                                                                                                         151
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27,
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D74E0C89082A9788 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of more than 15,000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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Q8WUK1;

PRELIMINARY;

PRT;

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RC TISSUE-Primary B-Cells;

RX MEDLINE-22388257; PubMed-12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max.

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., KocEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards S., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                          Query Match
Best Local S
Matches 86
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InterPro; IPR0031597; Ig_cl.
InterPro; IPR0031597; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam. PP07654; Cl-set; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, BC02024
PIR, F36005;
PIR, G36005;
PIR, PH1642;
PIR, PH1645;
PIR, PH1646;
PIR, PH1646;
PIR, PH10098;
PIR, PL0098;
PIR, PL0098;
PIR, PL0098;
PIR, S31119;
PIR, S31119;
PIR, S31119;
PIR, S31119;
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01-MAR-2002
01-MAR-2004
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata,
Mammalia, Eutheria, Primates;
                                                                                                                                                                                                                                                                                                                                                            Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (DEC-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                 PROSITE; PS50835; IG LIKE;
PROSITE; PS00290; IG MHC; I
SEQUENCE 613 AA; 67295 I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse cDNA sequences.";
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PF00047; ig; 1.
; SM00406; IGv; 1.
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86; Conser
                                                                                 NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCA-SWIS--DFFDYWGQGTLVTVSS
ADSVKGRFT1SRDNSKNTLYLQMNSLRAEDTAVYYCAKDWSEGVETFD1WGQGTMVTVSS
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(TrEMBLrel.
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nilarity 70.5%;
Conservative
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G36005.
PH1642.
PH1643.
PH1646.
PH1098.
P10120.
S15190.
S31119.
S31119.
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                                                                                                                                                                                                                                                                 UNKNOWN 3.
MW; 60C7F5950671E315 CRC64;
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Last annotation updat
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                                                                                                                                                                        Score 424.5; DB 2
Pred. No. 2.8e-36;
B; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Search completed: December 29, Job time: 133.79 secs
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Best Local S
Matches 82
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02-MAR-2004
02-MAR-2004
02-MAR-2004
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                                                                                                                                                                                                                                     gamma3 in vivo repertoires."
Submitted (SEP-2002) to the I
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                            BAD00531
                                                                                                                                                                                                                             EMBL; AB092169; BAD00531.1;
                                                                                                                                                                                                                                                            Honda T., Akahori Y., Kurosawa Y.; "Libraries of heavy-chain antibodies reflecting
                                                                                                                                                                                                                                                                                     IISSUE≃Spleen;
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                          Camelus dromedarius
                                                                                                                                                                                                                                                                                                                                                                      IGVH
                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
                                               61
                                                                       61
                                                                                                                                             82;
                                                                                                                                                       Similarity
                                                                    NQRFKGRFTISLDKSKRTAYLOMNSLRAEDTAVYYCASWISDFFDYWGQGTLVTVSSAS 119
                                                                                                          EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.
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S
                                               ADSVKGRFTISRDNAKEMVYLQMNSLKPEDTAVYYCVKWGDFSMDYWGEGTLVTISSES
                                                                                             EVQLVESGGGLVQPGGSLRLSCIASGFTFTGSWMWWVRQAPRKGLEWVSLINPSGSSTNY
                                                                                                                                                                                          120 AA;
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(TTEMBLrel. 27, Last sequence update)
(TTEMBLrel. 27, Last annotation update)
lin heavy chain VHDJ region (Fragment).
                                                                                                                                                                                                      120
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                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Tylopoda; Camelidae; Camelus
                                                                                                                                                                                         13277 MW;
                                                                                                                                                       66.9%;
              2004, 19:31:33
                                                                                                                                          ; Score 424; DB
; Pred. No. 4.8e
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                       4.8e-37
                                                                                                                                                                    DB 2;
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                                                                                                                                             30;
                                                                                                                                                                   Length
                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                               camel
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 sur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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 Pred. No. is t
score greater
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428.5
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427.5
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431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match
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Gapop 10.0 ,
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634
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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S31107

Ig heavy chain - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Ancession: S31107

R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma Eur. J. Immunol. 22, 247-251, 1992

A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple A;Reference number: S31104; MUID:9211633; PMID:1730252

A;Accession: S31107
            A;Cross-references: EMBL:X62955
A;Note: the nucleotide sequence was submitted to C;Superfamily: immunoglobulin V region; immunoglo C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                      A;Status: preliminary; nucleic acid sequence
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
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ALIGNMENTS

S31598 Ig heavy chain V region - human C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 C;Accession: S31598 C;Accession: S31598 R;Cuishinter, A.M.; Gauthier, L.; Boubli, L.; Pougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992 submitted to the EMBL Data Library, June 1992 A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-135 <CUI> A;Cross-references: EMBL:Z14170; NID:g31001; PIDN:CAA78539.1; PID:g31002 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;31-114/Domain: immunoglobulin homology <IMM> A; Reference number: S31585 A; Accession: S31598 A; Description: Mechanisms that generate human immunoglobulin diversity operate from 61 NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCA--SWISDFFDYWGQGTLVTVSS 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY h 70.3%; Similarity 74.8%; ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKISWEVSRFDYWGQGTLVTVSS QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYY Conservative Score 446; DB 2; Pred. No. 2.2e-34; 5; Mismatches 23 23; Indels Length 135; 2. Gaps 117 76 60

the

mitted to the EN immunoglobulin

EMBL Data in homology

Data Library, October 1991

not shown; translation

not

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Ig heavy chain V region (M43) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998 C;Accession: D36005 R;Schroeder Jr., H.W.; Wang, J.Y. Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990 A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable A;Reference number: A36005; MUID:90349571; PMID:2117273 A;Accession: D36005
                                                                                                                                                                                                                                                                                 R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: C36005
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A; Cross-references: GB:M18513
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A;Molecule type: mRNA
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A;Map position: 14932.33-14932.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
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  EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
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Pred. No. 1.1e-33;
9; Mismatches 22
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Pred. No. 4.5e-34;
7; Mismatches 22
                                        Score 437; DB 2;
Pred. No. 1.3e-33;
7; Mismatches 21
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Ig heavy chain V region (M74) - human (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-JC;Accession: G36005  
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A;Title: Preferential utilization of conserved immunoglobulin heavy A;Reference number: A36005; MUID:90349571; PMID:2117273
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R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of the IgA and IgG rear
A;Reference number: S20765
A;Accession: S20782
                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
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C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-124 < MOR>
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                                                                                                                                     F;15-98/Domain:
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71.9%;
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                                                         Score 436; DB 2; 1
Pred. No. 1.6e-33;
6; Mismatches 24;
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Pred. No. 1.5e-33;
0; Mismatches 21
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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31686
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-140 <CUI>
A; Residues: 1-140 <EUI>
A; Cross-references: EMBL: Z14205; NID: g30969; PIDN: CAA78574.1;
C; Superfamily: immunoglobulin V region; immunoglobulin homolog
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: S31686
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S31114
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EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIH#VRQAPGKGLEWVASINPDYDITNY
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                                                                  Score 436; DB
Pred. No. 1.9e
9; Mismatches
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Pred. No. 1.7e-33;
B; Mismatches 19
                                                                                                                                                      <MM>
                                                                                      DB 2;
1.9e-33;
                                                                  21;
                                                                                                           Length 140;
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-132 <CUI>
A;Residues: EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; PID:g31000
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-113/Domain: immunoglobulin homology <IMM>
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A;Description: Mechanisms that generate human immunoglo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region - human (;Species: Homo sapiens (man) (;Species: Homo sapiens (man) (;Date: 0)-Mar.1994 #Bequence_revision 10-Nov-1995 #text_change 23-Jul-1999 (;Accession: S31603
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A;Status: preliminary; nucleic acid sequence
A;Molecule type: mRNA
A;Molecule type: mRNA
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C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Dates ion: S31103
R;Raaphorst, F.M.; Timmers, B.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.P.
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and short diverse the Restricted utilization of germ-line V(H)3 genes and genes 
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A; Accession: S31603
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                                                                                               EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
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72.3%;
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                                                                                                                                                                                                                     Score 435; DB 2;
Pred. No. 2.2e-33;
8; Mismatches 24
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Pred. No.
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RESULT 13
S31588
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C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
C;Accession: $46390
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <MAH>
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A;Molecule type: DNA
A;Residues: 1-114 <FIG>
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A;Title: In vitro assembly of repertoires of antibody chains A;Reference number: S46390; MUID:94254092; PMID:8196048
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                                                                                                                      ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRGFW-SGYKDYWGQGTLVTVS
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71.9%;
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Pred. No. 2.2e-33;
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Pred. No. 2.1e-33;
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RESULT 15
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F;15-98/Domain:
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A; Residues: 1-128 < MOR>
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   precursor V region (mu)
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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31588
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
B;Description: Mechanisms that generate human immunoglobulin diversity oper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W. Eur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage A;Reference number: S26786; MUID:92111632; PMID:1730251
A;Accession: S26786
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A;Residues: 1-140 <CUI>
A;Cross-ferences: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
A;Cross-ferences: EMBL:Z14200; nimunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGLYCSSTSCYIMSNNWFDPWGQ
                                                                                                                                         1 EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
                                                   NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCAS-----
                                                                                                            OVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSSSYTNY
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; Pred. No. 2.9e-33;
10; Mismatches 18
                                                                                                                                                                                                                                                   Score 433.5; DB Pred. No. 3e-33;
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human (fragment)

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C;Species: Homo sapiens (man)
C;C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Caccession: S70442
R;Culsinier, A.M.; Fumoux, F; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgW kappa/lambda EBV human B cell clone: an early step of differentiation of fell immunol. 29, 1363-1373, 1992
A;Reference number: S70442; MUID:93024508; PMID:1383695
A;Recession: S70442
A;Status: not compared with conceptual translation
A;Kolecule type: mRVA
A;Residues: 1-140 <CUI>A;CUISE (UNIPROT:QBWUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMMN
Query Match
Best Local Similarity 72.5%; Pred. No. 3.3e-33;
Matches 87; Conservative 7; Mismatches 23; Indels 3; Gaps 1;
Db 20 VQLVESGGGUVQPGGSLRLSCATGGYTFTEXIIHWYRQAPGKGLEWVAFIRYDGSNKYY 79

OY 1 EVOLVESGGGUVQPGGSLRLSCATGGYTFTEXIIHWYRQAPGKGLEWVAFIRYDGSNKYY 79

OY 61 NQRFKGRFTISLDKSKRTAXLOMNSLRABDTAVYYCAS---WISDFFDYWGQGTLVTVSS 117
Db 80 ADSVKGRFTISRDNSKNTLYIQMNSLRABDTAVYYCARDHIVGATYFDYWGQGTLVTVSS 139

Search completed: December 29, 2004, 19:36:35
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Result
No.
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Maximum |
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Maximum Match 100%
'Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB seq length: 0
DB seq length: 2000000000
                                             Score
                                                                                                                                                                                                                                                634
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
        Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1599051 seqs, 359727711 residues
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634
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                                                                                                                                                                                                                                                                                                         Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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    14 US-01-044-896-5
15 US-01-940-166A-1
15 US-01-762-967-1
16 US-09-940-166A-1
17 US-09-940-166A-1
18 US-09-940-166A-1
19 US-09-940-166A-1
19 US-10-227-694-2
10 US-10-762-967-7
14 US-10-762-967-7
15 US-10-762-967-7
16 US-10-762-967-7
17 US-10-815-84-12
17 US-10-815-641-23
14 US-10-815-641-23
15 US-10-818-765-4
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Sequence 5, Appli
Sequence 10, Appl
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Sequence 1, Appli
Sequence 1, Appli
Sequence 7, Appli
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•	461.5	•	61.	461.5	61	61	461.5	61	462	462	463	463	463	463	468.5	470	473	477.5	477.5	477.5	477.5	477.5	480.5	481	484.5	487	487	487	487	487	487
72.8	72.8	72.8	•	•	•	•	72.8	•	•	72.9	•	•	•	73.0	73.9	•	•	75.3			•	•	75.8			ა	ა.	9	76.8	٥,	76.8
628	527	472	449	449	449	449	449	228	119	119	470	470	225	225	122	121	121	452	298	256	253	253	122	451	122	119	119	119	119	119	119
17	15	17	5	14	14	14	14	14	14	14	14	14	16	14	17	10	5	10	10	10	10	10	17	14	17	17	16	15	15	14	9
US-10-723-003-58	-10-18	-723-003-	-659-825-	3-299-	6-974-	-316-694-	-10-253-366-	-10-36		US-10-267-286A-13	US-10-227-694-5		-10-379-392-	-364-953-1	-10	-09-795-798-	-09-795-798-	-09-726-258-	-09-726-258-	-09-726-258-7	-09-726-258-	-09-726-258-5	-10-835-641-2	-10-423-299-	-10-818-765-	-10-719-310-	0-619-754-	-10-600	-10-608	S-10-268-50	US-09-811-123-2
8, App	Sequence 25, Appl	e 54, App	e 2, Appl	'n	e 2	e 2,	'n		e 14	e 13	æ	9	17	12	26	Sequence 24, Appl	ū	71	60	e 70	55	ស្ល	20	Ф 4	N	Sequence 4, Appli	4	Η	4	equence 4	Sequence 2, Appli

ALIGNMENTS

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APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Jin K.
APPLICANT: Stewart, Timothy
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
FILE REFERENCE: GENERIT.074A
CURRENT APPLICATION NUMBER: US/10/044,896
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: 60/270775
PRIOR APPLICATION NUMBER: 60/270775
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""" OTHER INFORMATION: This sequence represents a humanized chimeric; OTHER INFORMATION: antibody comprising human and non-human seque;
                                                                                                                                                                                                                         US-10-044-896-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-044-896-5
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 119
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10044896 Publication No. US20030166228A1 GENERAL INFORMATION:
                                                                                                                                                            Best
                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
61 NORFKGRFTISLDKSKKTAYLOMNSLRAEDTAVYYCASWISDFFDYWGOGTLVTVSSAS 119
                                                           h 100.0%; Score 634; DB 14; Similarity 100.0%; Pred. No. 1.8e-50; 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                          non-human sequences.
                                                                                                                                         Indels
                                                                                                                                                                            Length 119;
                                                                                                                                         0,
                                                                                                                                         Gaps
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RESULT 3
US-10-404-286-10
is Sequence 10, Application US/10404286
publication No. US20040057951A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. US20020081294A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/251652
FILING DATE: 17-FEB-2000
APPLICATION NUMBER: 08/788800
FILING DATE: 22-JAN-1997
APPLICATION NUMBER: 60/093038
FILING DATE: 23-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/811,384
FILING DATE: 20-Dec-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1729C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEPHONE: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas, G. Roger
Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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ADDRESSEE: Genente
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                                                                                                                                       121
                                                                                                                                                                         114 TVSSAS 119
                                                                                                                                                                                                              61 NORFMDRFTISVDKSTSTÄYMOMNSLRÄEDTÄVYYCÄRWRGLNYGFDVRYFDVWGQGTLV 120
                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                             l Similarity
97; Conserv
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                                                                                                                                                                                                                                                                                                           EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
                                                                                                                                       TVSSAS 126
                                                                                                                                                                                                                                   NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCASWIS-----DFFDYWGQGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 232 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                         78.8%; ilarity 77.0%; Conservative
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Pred. No. 7.3e-38;
7; Mismatches 15
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                   ; Sequence 1, Application US/09940166A
; Patent No. US20020058324A1
; GENERAL INFORMATION:
   APPLICANT: Blank, Gregory S.
   Narindray, Daljit S.
   Zapata, Gerardo A.
   TITLE OF INVENTION: Protein Recovery
   NUMBER OF SEQUENCES: 7
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Best Local Similarity
Matches 97; Conserv
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           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                121 TVSSAS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.8%;
77.0%;
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy di
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/10/404,286
FILING DATE: 31-Mar-2006
FILING TATE: 31-Mar-2006
CLASSIFICATION CAMPER: OS/611264
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/811384
FILING DATE: 20-DEC-2000
APPLICATION NUMBER: 09/251652
FILING DATE: 17-FEB-2000
APPLICATION NUMBER: 08/788800
FILING DATE: 22-JAN-1997
APPLICATION NUMBER: 60/093038
FILING DATE: 23-JAN-1996
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Evans, David W.
REGISTRATION NUMBER: NONE
REFERENCE/DOCKET NUMBER: P1729C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas, G. Roger
Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
                                61 NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCASWIS-----DFFDYWGQGTLV 113
61 NORFMORFTISVDKSTSTAYMOMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV
                                                                                                                              1 EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY 60
                                                                                                1 EVOLVESGGGLVOPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech,
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881
                                                                                                                                                                                           Pred. No. 7.3e-38;
7; Mismatches 15
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US-10-762-967-1
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10762967 Publication No. US20040138426A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.8%;
Best Local Similarity 77.0%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/097,309
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/940,166A
FILING DATE: 27-Aug-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    Zapata, Gerardo A. TITLE OF INVENTION: Protein Recovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Blank, Gregory S.
Narindray, Daljit S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TVSSAS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                      STATE: California
                                                                                                                                                                                           STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                  ZIP: 94080
                                                                                                                                                    COUNTRY: USA
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Pred. No. 7.6e-38;
7; Mismatches 15;
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RESULT 6
US-09-940-166A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09940166A Patent No. US20020058324A1 GENERAL INFORMATION:
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                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/940,166A

FILING DATE: 27-AUG-2001

CLASSIFICATION: «UDKnown»

PRIOR APPLICATION NUMBER: 09/097,309

PILING DATE: 13-JUN-1997

ATTORNEY/AGENT INFORMATION:
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FILING DATE: 21-Jan-2004
CLASSIPICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/097,309
FILING DATE: 12-Jun-1998
APPLICATION NUMBER: 60/050951
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Blank, Gregory S.
Narindray, Daljit S.
Zapate, Gerado A.
TITLE OF INVENTION: Protein Reco
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REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TVSSAS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                   CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1 DNA Way
NAMB: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
                                      NAME: Schwartz,
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genentech,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 499.5; DB 1
Pred. No. 7.6e-38;
7; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                       Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recovery
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FILE REFERENCE: P1867R1
CURRENT APPLICATION NUMBER: US/10/227,694
CURRENT FILING DATE: 2002-08-26
FRIOR APPLICATION NUMBER: US 60/315,209
PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 2
LENGTH: 300
US-10-762-967-7
; Sequence 7, Application US/10762967
; Publication No. US20040138426A1
; GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
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US-10-227-694-2
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                                                                                       RESULT 8
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10227694
Publication No. US20030077739A1
GENERAL INFORMATION:
APPLICANT: Simmons, Laura
APPLICANT: Andersen, Dana
TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 78.8%;
Best Local Similarity 77.0%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                      NORFMORFTISVOKSTSTAYMOMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV 143
                                                                                                                                                                                                                                                                     EVOLVESGGGLVQPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSH
                                                                                                                                                                                                                                                                                                  EVOLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                              78.8%;
77.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                  Score 499.5; DB 14;
Pred. No. 9.5e-38;
7; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 499.5; DB 9
Pred. No. 9.5e-38;
7; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length 300;
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US-09-811-384-12
(S-09-811-384-12
; Sequence 12, Application US/09811384
; Patent No. US20020081294A1
; GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/10/762,967
PILING DATE: 21-Jan-2004
CLASSIFICATION : CURKOWN>
PRIOR APPLICATION NUMBER: US/09/097,309
APPLICATION NUMBER: US/09/097,309
APPLICATION NUMBER: US/09/097,309
FILING DATE: 12-JUN-1998
APPLICATION NUMBER: 60/050951
PILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                     APPLICANT: Bednar, Martin M.
Thomas, G. Roger
Gross, Cordell B.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Narindray, Daljit S.
Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97;
                                                                                                                                                                                                                                                                                                                                                                                                                          84 NORFMORFTISVDKSTSTAYMOMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGOGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCASWIS------DFFDYWGQGTLV 113
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                       STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acid
                 STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                 South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.8%;
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Pred. No. 9.5e-38;
7; Mismatches 15
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83 60

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RESULT 10
US-10-404-286-12
; Sequence 12, Application US/10404286
; Publication No. US20040057951A1
; GENERAL INFORMATION:
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/251652
FILING DATE: 17-FEB-2000
APPLICATION NUMBER: 08/788800
FILING DATE: 22-JAN-1997
APPLICATION NUMBER: 60/093038
FILING DATE: 23-JAN-1996
ATTORNEY/ACENT INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/404,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                     APPLICANT: Bednar, Martin M.
Thomas, G. Roger
Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1729C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVSSAS 126
                                                                                                                                                                                               ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVOLVESGGGLVQPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSH 60
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                                                                                                                                                         ZIP: 94080
                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650/952-9881
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77.0%;
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Pred. No. 1.4e-37;
7; Mismatches 15;
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US-10-835-641-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application US/10835641 Publication No. US20040236078A1 GENERAL INFORMATION:
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Matches 97; Conservative
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1739
TELEPAX: 650/92-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA;
APPLICATION NUMBER: 09/811384
FILING DATE: 20-DEC-2000
APPLICATION NUMBER: 09/251652
FILING DATE: 17-FEB-2000
APPLICATION NUMBER: 08/788800
PILING DATE: 27-JAN-1997
APPLICATION NUMBER: 60/093038
FILING DATE: 27-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: RVANE: DAYAG
                                                                                                                                                                                                                                                                                                                                                                     Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech The
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/705,398
FILING DATE: 02-Nov-2000
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/835,641
FILING DATE: 30-Apr-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                COUNTRY: USA
ZIP: 94080
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                                                                         CITY: South San Fi
STATE: California
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: 1 DNA Way
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Evans, David W. REGISTRATION NUMBER: NONE
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77.0%;
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Pred. No. 1.4e-37;
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RESULT 13
US-10-818-765-4
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Sequence 4, Application US/10818765
                                                                                                                                                                                                                                                                 Query Match
Best Local S
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Publication No. US20030166228A1
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Jin K.
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 77.0 Matches 97; Conservative
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Best Local
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APPLICANT: Stewart, Timothy
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: ANTI-INTERPERON-ALPHA ANTIBODIES
FILE REFERENCE: GENENT.074A
CURRENT APPLICATION NUMBER: US/10/044,896
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: 60/270775
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 119
TYPE: PRT
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/715272
FILING DATE: 14-UN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                                                                                              61 NORFKGRETISLDKSKRTAYLOMNSLRAEDTAVYYCASWISDFFDYWGOGTLVTVSSAS 119
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                                                                                         NQRFKGKATLTLDKSSRTAYLELRSLTSEDSAVYYCASWISDFFDYWGQGTTLMVSAAS 119
                                                                                                                                                                 EVQLQQSGPELVKPGASVKISCKTSGYTFTEYIIHWVKQGHGRSLEWIGSINPDYDITNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NORFMORFTISVOKSTSTAYMOMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 650/225-1994
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                                                                                                                                                                                                                                                   Conservative
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77.0%;
                                                                                                                                                                                                                                                             77.8%; Score 493; DB 14; Length 119; 73.1%; Pred. No. 1.4e-37;
                                                                                                                                                                                                                                             17; Mismatches
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Pred. No. 1.5e-37;
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TITLE OF INVENTION: ANTHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
FILE REFERENCE: GENENT.073A2
CURRENT APPLICATION UNMER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
FRIOR APPLICATION NUMBER: 60/238,327
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTMARE: FASESEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COULED THEOREMETICAL HUMBER: 05 SETURES:
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                                                                                                                                                                                                                       j OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-811-123-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: humanized sequence US-10-818-765-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication No. US20040202658A1 GENERAL INFORMATION:
                                                                                                                                            Matches
                                                                                                                                                            Query Match
Best Local S
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Patent No. US20020001587A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
LENGTH: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Benyunes, Mark C.
TITLE OF INVENTION: THERAPY OF AUTOIMMUNE DISEASE IN A PATIENT WITH AN TITLE OF INVENTION: INADEQUATE RESPONSE TO A TWF-a INHIBITOR FILE REFERENCE: P2027R1-US
CURRENT APPLICATION NUMBER: US/10/818,765
CURRENT FILING DATE: 2004-04-06
PRIOR APPLICATION NUMBER: US 60/461,4819
PRIOR PILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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61 NQRFKGRFTISLDKSKKTAYLQMNSLRAEDTAVYYCASWI--SDFFDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NQKFKGRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSNSYW----YFDVWGQGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCAS-----WISDFFDYWGQGTL
                                                             1 EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIY
                                                                                                                                            93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
                                                                                 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY
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97; Conserva
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78.2%;
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                                                                                                                                        Score 487; DB 9;
Pred. No. 5.1e-37;
1; Mismatches 13
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Pred. No. 6.3e-37;
6; Mismatches 13;
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                                                                                                                                                                               Length 119;
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RESULT 15

US-10-268-501-4

US-10-268-501-4

US-10-268-501-4

Sequence 4, Application US/10268501

Publication No. US20030086924A1

APPLICATION: Sliwkowski, Mark X.

APPLICATION UNDERER: US/10/268,501

CURRENT PILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/602,812

PRIOR FILING DATE: 2002-06-25

NUMBER: OF EQ ID NOS: 13

SEQ ID NO 4

LENGTH: 119

TYPE: PRI

TYPE: PRI

OTHER INFORMATION: Humanized VH sequence

US-10-268-501-4

Query Match

ONE JS: 18-50-14

Query Match

ONE JS: 18-50-14

ONE JS: 18-50-
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sequence

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfIles1.pep:*
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            GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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PCT-US93-07832-29
US-08-38-373C-30
US-08-437-642B-30
PCT-US93-07832-30
PCT-US93-07832-30
PCT-US93-07832-30
PCT-US93-07832-31
US-09-097-309-1
US-09-097-309-1
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US-09-097-171A-1
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US-09-460-587-7
US-09-460-587-7
US-09-460-587-7
US-09-460-587-7
US-09-460-587-3
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Sequence 27, Appl
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Sequence 29, Appl
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                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/934,373C

FILING DATE: 21-Aug-1992

CLASSIFICATION NUMBER: PCT/US92/05126

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

PRIOR APPLICATION NUMBER: PCT/US92/05126

PRIOR APPLICATION NUMBER: 97/15272

PRIOR APPLICATION NUMBER: 07/15272

PRIOR APPLICATION NUMBER: 07/25272

PRIOR APPLICATION NUMBER: 07/15272

PRIOR APPLICATION NUMBER: 07/152
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US-07-934-373C-27
                                                       Query Match
Best Local Similarity
Matches 98; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/07934373C Patent No. 5821337 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
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US-07-938-373C-28
US-07-939-07832-28
US-07-934-373C-26
US-08-437-642B-26
US-07-934-373C-38
US-07-934-373C-38
US-07-934-373C-35
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                                                          Score 503.5; DB 2;
Pred. No. 4.4e-42;
6; Mismatches 15;
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US-08-437-642B-27
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                                                                                                                      Matches
                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                         TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                     NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: PO-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/715272 FILING DATE: 14-JUN-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOPTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 17-NOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPTUDES WISELES (PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
ZIP: 94080
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South San Francisco
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                                                                  EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDVDITNY 60
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                                                                                                                      Conservative
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77.8%;
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                                                                                                                   Score 503.5; DB 3
Pred. No. 4.4e-42;
6; Mismatches 15
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PCT-US93-07832-27
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TELEX: 910/371-7168
TELEX: SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
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                                                                                                                                                                                                                    Matches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07:
FILING DATE: 1930820
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/715272
FILING DATE: 14-UN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05:
APPLICATION NUMBER: PCT/US92/05:
PRIOR APPLICATION DATA:
APPLICATION DATA: 07/934373
APPLICATION UMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/934373
FILING DATE: 21-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 70
REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                             LENGTH: 232 amino acids
TYPE: amino acid
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CITY: South San Francisco
                                                                                                                                                                                                                                     Local
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121 TVSSAS 126
                                  114 TVSSAS 119
                                                                                             61 NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCASWIS------DFFDYWGQGTLV 113
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                                                                      61 NQREMDRETISVDKSKNTLYLQMNSLRAEDTAVYYCARWRGLNYGEDVRYEDVWGQGTLV 120
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98; Conservative
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                                                                                                                                                                                                                                  79.4%;
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RESULT 4 US-07-934-373C-29

Sequence 29, Application US/07934373C Patent No. 5821337

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                                                       Sequence 10, Application US/08788800
Patent No. 5914112
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell B.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: Paul J Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
PILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94060
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COMPATTING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING UALL S3U CLASSIFICATION: 53U PRIOR APPLICATION DATA: PCT/US92/05126 APPLICATION NUMBER: PCT/US92/05126 APPLICATION NUMBER: 15-JUN-1992
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OPERATING SYSTEM: PC-D
SOFTWARE: WinPatin (Ges
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 232 amino acids
TYPE: Amino Acid
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CITY: South San Francisco
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US-08-437-642B-29
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US-08-788-800-10
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Patent No.
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TELEPAX: 415/952-9881
TELEX: 910/371-7158
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acide
TYPE: Amino Acid
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
                                                                                                                                                                                                                                                                                                                           APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKST NUMBER: PO:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                              CITY: South San Francisco
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STATE: California
COUNTRY: USA
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o. 6054297
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97; Conservative
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Pred. No. 1.1e-41;
7; Mismatches 15;
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INFORMATION FOR SEQ ID NO: 29
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Applicat GENERAL INFORMATION:
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
PILING DATE: 19930820
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Genentech, inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 650/225-1994
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ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
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APPLICATION NUMBER: 08/14
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
APPLICATION NUMBER: 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
PILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
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Local Similarity 77.0%;
nes 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
APPLICATION NUMBER: 07/934373 FILING DATE: 21-AUG-1992
                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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Pred. No. 1.1e-41;
7; Mismatches 15;
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RESULT 8
US-07-934-373C-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5821337
GENERAL INFORMATION:
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Best Local Similarity
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
                                                                                                                                                                        APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-UUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
                                  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 70: REFERENCE/DOCKET NUMBER: 70: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
COMPUTER: IBM PC comp
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acio
                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: PO'
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94080
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                                                                   TELEPHONE:
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 235 amino acids
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                                                                     650/225-1994
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77.0%;
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US-08-437-642B-30
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                                                      US-08-437-642B-30
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Matches 97, Conservative
                    Query Match
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 Best Local Similarity
                                                                                                      TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: 07/934373
APPLICATION NUMBER: 07/934373
PILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: 08/146206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: PO-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/7:
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PCT/US92/05126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/1 FILING DATE: 17-NOV-1993
                                                                          TOPOLOGY:
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South San Francisco
California
                                                                                     amino Acid
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77.0%;
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Pred. No. 1.1e-41;
7; Mismatches 15
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Score 499.5; DB 3; Pred. No. 1.1e-41;
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                Length 235;
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PCT-US93-07832-30
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                                                                                                                                 Matches
                                                                                                                                                               Query Match
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715
FILING DATE: 14-JUN-1991
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS LENGTH: 235 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Genentech, Inc. TITLE OF INVENTION: Immuno
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 7
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 15.JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
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CORRESPONDENCE ADDRESS:
                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                 97;
                                                                                     1 EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY 60
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NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCASWIS------DFFDYWGQGTLV 113
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                                                                  EVQLVESGGGLVQPGGSLRLSCATSGYTFTBYTMHWMRQAPGKGLEWVAGINPKNGGTSH
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                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 Kb floppy disk
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                                                                                                                                                 Score 499.5; DB 5;
Pred. No. 1.1e-41;
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                                                                                                                              Mismatches
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                                                                                                                                 Indels
                                                                                                                                                               Length 235;
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Best Local S
Matches 97
Sequence 1, Application US/09097171A
Patent No. 6171586
GENERAL INFORMATION:
APPLICANT: Lam, Xanthe M.
APPLICANT: Oeswein, James Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09097309 Patent No. 6121428
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APPLICATION NUMBER: 60/050951
PILING DATE: 13-UUM-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Tinothy R.
REGISTRATION NUMBER: 32171
REPERENCE/DOCKET NUMBER: P1105R
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,309
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APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: South San Francisco
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                                                                                                                                                                                                      114 TVSSAS 119
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                                                                                                                                                                                                                                                                                                                                                                                                        78.8%;
77.0%;
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P1105R1
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 499.5; DB 3
Pred. No. 1.1e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 241;
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Matches
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Patent No. 6322997
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Best Local S
                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/874897
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P108
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                              APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEPAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WinPatin (Ge:
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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             CITY: South San FI
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
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COUNTRY: USA
                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                       61 NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCASWIS------DFFDYWGQGTLV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97;
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97; Conservative
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I: Weissburg, Robert P.
F: Wong, Rita L.
INVENTION: Antibody Formulation
                                                  1 DNA Way
USA
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Shahrokh, Zahra
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                                                                 Genentech, Inc.
                              Francisco
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77.0%;
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Pred. No. 1.1e-41;
7; Mismatches 15;
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RESULT 14
US-09-940-166A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09940166A Patent No. 6716598 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,166A
PILING DATE: 27-Aug-2001
CLASSIFICATION - CUNKNOWN>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 241 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Blank, Gregory S.

Narindray, Daljit S.
Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TVSSAS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 78.8%; Score 499.5; DB 3; Similarity 77.0%; Pred. No. 1.1e-41;
                                                                                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NORFMORFTISVOKSTSTAYMOMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NORFKGRFTISLDKSKRTAYLOMNSLRAEDTAVYYCASWIS-----DFFDYWGQGTLV 113
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                                                                                                                                                                                                                                                           ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                  STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                    COUNTRY: USA
APPLICATION NUMBER: 09/097,309 FILING DATE: 13-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Patent No. 6121428
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
APPLICANT: Tapata, Gerardo A.
ITITLE OF INVENTION: Protein Recov.
NUMBER OF SEQUENCES: 7
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US-09-097-309-7
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                    TRLEPAX: 650/300 TRLEPAX: 650/300 TRLEPAX: 650/300 TRLEPAX FOR SEQ ID NO: 7 SEQUENCE CHARACTERISTICS: SEQUENCE 300 mino acids
                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097
FILING DATE: 12-JUN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/050951
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P110
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
LENGTH: 300 amin
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
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Protein Recovery

60/050951

P1105R1

US/09/097,309

1.44 Mb floppy disk

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Best Local Similarity 77.0 Matches 97; Conservative
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                        114 TVSSAS 119
121 TVSSAS 126
                                                                                   61 NQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV 120
                                                                                                            61 NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCASWIS------DFFDYWGQGTLV 113
                                                                                                                                                                                                  1 EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYIIHWVRQAPGKGLEWVASINPDYDITNY 60
                                                                                                                                                                       1 EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSH 60
                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                 78.8%;
77.0%;
                                                                                                                                                                                                                                                           Score 499.5; DB 4
Pred. No. 1.1e-41;
7; Mismatches 15
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2013s:*
6: geneseqp2013as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Adj88007 Humanised	Ade71453 Humanise	Aau74540 Human ant		Aab60399 Humanised	Aab62086 Humanised	Aae28147 Murine 9F	Aar30775 pH52-8.0	Aab03664 Anti-CD18	Adk18343 Amino aci		Aay08755 Human IgG	Aaw34505 Heavy cha		Aab66785 Protein e	Aaw30635 Recombina	Aaw95623 pS1130 ex	Aaw30631 Recombina	Aab66776 rhuMAb CD	Aaw95614 Humanized	Adk18341 Amino aci	Abg31888 Humanised	Aay08753 Human ant	Aaw34503 Heavy cha	manie	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
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Aab30321	Aay77765	Aay29457	Aaw69304	Aae39086	Aae39089	Abu59504	Abu59506	Abu13793	Abu13791	Aab30314	Aab30316	Aay77759	Aay77757	Aay29454	Aay29444	Aar30772	Adf11670	Adp43327	Adn12053
Humanised	Humanised	6G4V11N35	Humanised	6G4-2-5V1	Humanised	Humanised	Humanised	Humanised	huxCD3v9,	anti-CD11	Humanised	Variable							

ALIGNMENTS

AAE28150; Humanised 9F3 version 13 (V13) heavy chain variable domain. 27-DEC-2002 AAE28150 standard; protein; 119 (first entry) ₹

Human; interferon alpha; IFNalpha; insulin-dependent diabetes mellitus; autoimmune disease; systemic lupus erythematosus; autoimmune thyroiditis; antibody therapy; immunosuppressive; antiinflammatory; dermatological; 9F3 monoclonal antibody; heavy chain variable domain.

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99. .106 Location/Qualifiers 26. .35 note= note= "Complementarity "Complementarity determining region 3 (CDR3)" determining determining region 1 region 2

(CDR2) " (CDR1) "

WO200266649-A2

29-AUG-2002.

29-JAN-2002; 2002WO-US002709

22-FEB-2001; 09-JAN-2002; 2001US-0270775P. 2002US-00044896.

(GETH) GENENTECH INC.

Chuntarapai A, Kim JK, Presta LG, Stewart

Η,

WPI; 2002-682767/73.

New anti-interferon alpha monoclonal antibody, 9F3, useful for treating autoimmune diseases e.g. insulin-dependent diabetes mellitus, systemic lupus erythematosus and autoimmune thyroiditis.

Disclosure; Page 98; 100pp; English.

The present invention relates to novel anti-interferon alpha (IFNalpha)

អនុស្តិតិស្តីស្ត្រិស្តី និង្គិតិស្ត្រី និង្គិតិស្ត្រី និង្គិតិស្ត្រី និង្គិតិស្ត្រី និង្គិតិស្ត្រី និង្គិតិស្ត

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This sequence represents the heavy chain of the humanised H52 antibody. The H52 antibody can be used in the method of the invention. The method is for treating focal ischaemic stroke, i.e. damage to the brain due to interrupted blood supply, in a mammal, caused by obstruction of a main cerebral artery, comprises administering anti-CD18 antibody to increase cerebral blood flow and/or reduce the size of the area of brain that
                                                                                                                                                                                                                                                           Administering an anti-CD18 antibody to treat focal ischaemic stroke -increasing cerebral blood flow and reducing size of brain infarct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised antibody; HuH52; heavy chain; focal ischaemic stroke; embolism; brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism; transient ischaemic attack; thrombolytic therapy; thrombosis; therapy; systemic hypoperfusion; cardiac arrest.
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arterial obstruction.

CD18,

This invention describes a method for improving the clinical outcome in focal ischaemic stroke by administering novel anti-CD18 antibody which

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;
cerebroprotective; cerebral artery obstruction; blood flow; infarct;
CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;
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UNIV VERMONT & STATE AGRIC COLLEGE.
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No. 4.2e-39;
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Best Local
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22-JAN-1997;
17-FEB-1999;
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                        The invention relates to a method or reducing infarct size in focal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          focal ischaemic stroke; main cerebral artery;
tissue plasminogen activator; anti-CD18 antibody; stroke;
acute ischaemic stroke; thrombolytic therapy;
Pabvlb salvage receptor binding epitope; thromboembolic stroke
                                                                                           Claim
                                                                                                                                    Increasing cerebral blood flow and/or reducing infarct size in ischemic stroke using anti-CD18 antibody and tissue plasminogen is useful to improve clinical outcome in acute ischemic stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; humanisec focal ischaemic
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                                                                                                                                                                                                                                                                                                                             GENENTECH
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97US-00788800.
99US-00251652.
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77.0%;
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                        of increasing cerebral k ischaemic stroke caused
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                        blood flow and/
d by obstruction
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The present flow and/or obstruction of the method co

present invention relates to a method for increasing cerebral blood w and/or reducing infarct size in focal ischaemic stroke caused by truction of a main cerebral artery in a mammal, particularly humans. method comprises co-administering tissue plasminogen activator (tPA

Claim 11;

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Increasing cerebral blood flow and/or reducing infarct size in ischemic stroke caused by obstruction of a main cerebral artery human comprises co-administering tissue plasminogen activator as

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Best Local
                                                                                                                                                                                  23-JAN-1996;
22-JAN-1997;
17-FEB-1999;
20-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasminogen activator and anti-CD18 antibody about 3-5 hours af stroke. The method is used to improve the clinical outcome in a ischaemic stroke and to provide an alternative to thrombolytic for treating thromboembolic stroke, particularly where thrombol therapy has been unsuccessful or is contra-indicated. The prese sequence represents a humanised H52 antibody (huH52) Fab, heavy used in the method of the invention
                                                                                                                                                                                                                                    31-MAR-2003;
                                                                                                                                                                                                                                                                            US2004057951-A1
                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                         cerebral artery;
humanised H52 ant
                                                                                                                                                                                                                                                                                                                                                             Cerebral blood flow;
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                                                                                                                                            Bednar
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                                                                                                                                                                                                                                                                                                Synthetic
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97US-00788800.
99US-00251652.
2000US-00811384.
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antibody;
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                                                                                                                                                               INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                 of humanised
                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.8%;
77.0%;
                                                                                                                                                                                                                                                                                                                                                             infarct size; focal ischaemic stroke;
                                                                                                                                            Thomas
                                                                                                                                                                                                                                                                                                                                      plasminogen activator; tPA; anti-CD18 huH52 Fab; stroke; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                            232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 499.5; DB 5;
Pred. No. 4.2e-39;
7; Mismatches 15;
                                                                                                                                           g
K
                                                                                                                                                                                                                                                                                                                                                                                 H52 (huH52) Fab heavy chain
                                                                                                                                            Gross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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heavy chain
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                                                                                                                                                                                                                                                                                                                                         vasotropic;
                                                                                                                                                                                                                                                                                                                                                   antibody;
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RESULT 6
AAW95614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc and anti-CD18 antibody to the mammal, where neither the tPA nor the anti-CC CD18 antibody is administered to the mammal until about 3-5 hours after the onset of focal ischaemic stroke. The anti-CD18 antibody is a CC chumanised H52 antibody (huH52 Pab). The anti-CD18 antibody binds to an CC extracellular domain of CD18 and inhibits or reduces the ability of a CC cell expressing CD18 to bind to endothelium. The anti-CD18 antibody binds CC CD18 with an affinity of 1-4 mm or less. The anti-CD18 antibody binds to the epitope bound by H52 antibody. The anti-CD18 antibody and the tPA are cell expressing cerebral body. The anti-CD18 antibody and the tPA are complex. The antibody and the tPA are complex to the mammal, or the anti-CD18 antibody is administered to the mammal, or the mathemal. The method is CC useful in increasing cerebral blood flow and/or reducing infarct size in CC coll ischaemic stroke caused by obstruction of a main cerebral artery in CC a human. The antibodies are particularly useful for treating stroke. CC unlike previous methods, the new method of treatment does not require CC prior administration of a thrombolytic agent to the mammal in order to CC undown an embolus/thrombus, and therefore increases cerebral blood flow and/or reduces infarct size. The present sequence represents the heavy creating for huH52 Fab.
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Best Local &
New stable aqueous antibody subjected to lyophilisation,
                                                                                WPI; 1999-080860/07
                                                                                                                                                                                                                                                              13-JUN-1997;
                                                                                                                                                                                                                                                                                                                   12-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus.
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                                                                                                                             Weissburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody; heavy chain; humanized; myocardial infarction; burns; thermal injury; ischemic; shock; ischaemic; haemorrhagic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanized anti-CD18 antibody rhuMAb CD18 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW95614 standard; protein; 241
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                                                                                                                                                                                                              (GETH ) GENENTECH INC
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97; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stroke.
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Pred. No. 4.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                           Shahrokh
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Best Local &
The present invention relates to a stable aqueous ph formulation, comprising an antibody not subjected to lyophilization, an acetate buffer of pH 4.8-5.5, a s polyol. The invention is useful for treating hemorrh injury, e.g. resulting from burns, stroke including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of the heavy chain of a humanized murine anti-CD18 antibody rhumab CD18. It can be used for the treament of disorders which include haemorrhagic shock, thermal injury (such as that resulting from burns), stroke (including ischaemic and haemorrhagic stroke) and myocardial infarction. The antibody formulation can be stabilised at a temperature of 2-8 deg. C for at least one year or at a temperature of deg. C for at least one stabilised stabilised at a temperature of 2-8 deg. C for at least one year or at a temperature of deg. C for at least one month and is stable following freezing and
                                                                                                                   Stable aqueous pharmaceutical formulation for treating hemorrhagic shock, thermal injury, stroke, and myocardial infarction, comprises an antibody
                                                                                                                                                                                                                                                                                                                                                                              Antibody; lyophilization; hemorrhagic shock; thermal injury; myocardial infarction; inflammation.
                                                                            Example 1, Fig 1, 56pp; English.
                                                                                                                                                         WPI; 2001-136863/14.
                                                                                                                                                                                  Weissburg
                                                                                                                                                                                                Lam XM,
                                                                                                                                                                                                                                                                           12-JUN-1998;
                                                                                                                                                                                                                                                                                                     09-JAN-2001.
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                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    rhuMAb CD18 heavy chain.
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                                                                                                       not subjected
                                                                                                                                                                                                                        (GETH )
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                                                                                                                                                                                                                        GENENTECH INC
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                                                                                                                                                                                Wong
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                                                                                                                 stroke, and
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77.0%;
                                                                                                                                                                                              Ongpipattanakul
                                                                                                       lyophilization.
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Pred. No. 4.4e-39;
7; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                               В,
                                                                                                                                                                                                Shahrokh
                                      pharmaceutical to prior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
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RESULT 8
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Best Local S
Matches 97
                A method has been developed for recovering a polypeptide comprising: (a) exposing a composition comprising a polypeptide to a reagent which binds to or modifies the polypeptide, where the reagent is immobilized on a solid phase; and (b) passing the composition through a filter bearing an opposite charge to the reagent so as to remove leached reagent from the composition. The present invention also describes a method for modifying a precursor antibody comprising a leucine zipper by exposing the precursor antibody to a protesse immobilized on a solid support so that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Region
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                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-060267/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant humanised
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                                                                                                                                                                                                                                 Fig 1A; 43pp;
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                                                                                                                                                                                                                                                                            for recovering part and filtering
                                                                                                                                                                                                                                                                                                                                                                                              Narindray
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242. .277
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       to a ]
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77.0%;
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                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leucine_zipper
                                                                                                                                                                                                                                                                               polypeptides from c
g to remove reagent.
                                                                                                                                                                                                                                                                                                                                                                                              Zapata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277
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Pred. No. 4.4e-39;
7; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₹
                                                                                                                                                                                                                                                                                                                                                                                              B
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                                                                                                                                                                                                                                                                                                    cell cultures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241;
port so that purify
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RESULT 9
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins from cell cultures. They are especially useful for isolating antibodies. The methods overcome the problem of reagent leakage into t protein as is the case in prior art immobilized modification systems. using a opposite charge filter the reagent can be excluded from the sample, preventing contamination. The present sequence represents the recombinant humanised anti-CD18 antibody (rhuMAb CD18) heavy chain, while used in an example from the present invention
                                                                                    New stable aqueous antibody subjected to lyophilisation,
                                                                                                                   WPI;
                                                                                                                                   Weissburg
                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                         AAW95623;
                                                                                                                                             Lam
                                                                                                                                                                                     13-JUN-1997;
                                                                                                                                                                                                       12-JUN-1998;
                                                                                                                                                                                                                            17-DEC-1998.
                                                                                                                                                                                                                                               WO9856418-A1
                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                        Mus musculus.
                                                                                                                                                                                                                                                                                                                           hemorrhagic;
                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody; heavy chain; humanized; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                  pS1130 expression
                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-1999
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                                                                                                                                                                  (GETH )
                                                                                                                                                                                                                                                                                                                                       ourns; thermal
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                                                                                                                 1999-080860/07.
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rg RP, Wong 1
                                                                                                                                                                  GENENTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCASWIS-----DFFDYWGQGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVSSAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NORFMORFTISVOKSTSTAYMOMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVQLVESGGGLVQPGGSLRLSCATSGYTPTEYIIHWVRQAPGKGLEWVASINPDYDITNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                                                                            stroke;
                                                                                                                                                                                                                                                                                                                     injury; 10 10 heavy
                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                        98WO-US012209
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1. .23
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                                                                                                                                                                  INC.
                                                                                                                                                                                                                                                                                                                                                                  cassette encoded rhuMAb CD18 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                     RL;
                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.8%;
77.0%;
                                                                                                                                             Ongpipattanakul
                                                                                                                                                                                                                                                                                                                                       ischemic;
                                                                                                                                                                                                                                                                                                                            chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 499.5; | Pred. No. 5.1e 7; Mismatches
                                                                                    formulations - comprising a buffer maintaining the
                                                                                                                                                                                                                                                                                                                                       shock; ischaemic; haemorrhagic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         499.5; DB 2
No. 5.1e-39;
                                                                                                                                              B
                                                                                                                                              Shahrokh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
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                                                                                    PH an
                                                                                                                                             Wang
                                                                                     antibody
at 4.5 -
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The sequence is that of the pS1130 encoded heavy chain of a humanize murine anti-CD18 antibody rhuMAb CD18. It can be used for the treame disorders which include haemorrhagic shock, thermal injury (such as resulting from burns), stroke (including ischaemic and haemorrhagic stroke) and myocardial infarction. The antibody formulation can be

humanized

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ent of that

Disclosure; Fig 21A; 87pp;

English

surfactant

and a polyol.

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RESULT 10
AAW30635
ID AAW30635
AC AAW30
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Best Local
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A method has been developed for recovering a polypeptide comprising: (a) exposing a composition comprising a polypeptide to a reagent which binds to or modifies the polypeptide, where the reagent is immobilized on a solid phase; and (b) passing the composition through a filter bearing an opposite charge to the reagent so as to remove leached reagent from the composition. The present invention also describes a method for modifying a precursor antibody comprising a leucine zipper by exposing the precursor antibody to a protease immobilized on a solid support so that
                                                                                                                                                                                                                                                                                          New method for recovering polypeptides from cell cultures with reagent and filtering to remove reagent.
                                                                                                                                                                                                                                             Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blank GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stabilised at a temperature of 2-8 deg. C for at least one year or at a temperature of 30 deg. C for at least one month and is stable following freezing and thawing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp.
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                                                                                                                                                                                                                                       Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NORFKGRFTISLDKSKRTAYLOMNSLRAEDTAVYYCASWIS-----DFFDYWGQGTLV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVSSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVSSAS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NORFMORFTISVOKSTSTAYMOMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Narindray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 humanised anti-CD18 antibody; rhuMAb CD18; leucine zipper; clonal antibody; muMAb H52; protein recovery; filtration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               humanised
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                                                                                                                                                                                                                                          4; 43pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US012334.
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                                                                                                                                                                                                                                          English.
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Pred. No. 5.5e-39;
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RESULT 11
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       The present invention relates to a stable aqueous pharmaceutical formulation, comprising an antibody not subjected to prior lyophilization, an acetate buffer of pH 4.8-5.5, a surfactant and polyol. The invention is useful for treating hemorrhagic shock, tinjury, e.g. resulting from burns, stroke including ischemic and hemorrhagic stroke, myocardial infarction, inflammatory disorders adult respiratory distress syndrome (ARDS), hypovolemic shock, ul colitis, rheumatoid arthritis and B-cell lymphomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the protease removes the zipper. The methods can be used to purify proteins from cell cultures. They are especially useful for isolating antibodies. The methods overcome the problem of reagent leakage into the protein as is the case in prior art immobilized modification systems. By using a opposite charge filter the reagent can be excluded from the sample, preventing contamination. The present sequence represents the recombinant humanised anti-CD18 antibody (rhuMAb CD18) heavy chain, which is used in an example from the present invention
                                                                                                                                                         Stable aqueous pharmaceutical formulation for treating hemorrhagic thermal injury, stroke, and myocardial infarction, comprises an ant not subjected to prior lyophilization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody; lyophilization; hemorrhagic myocardial infarction; inflammation.
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                                                                                                                                   Disclosure; Fig
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97; Conserv
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g RP, Wong
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                                                                                                                                 21; 56pp;
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Pred. No. 5.5e-39;
7; Mismatches 15
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shock, ulcerative
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RESULT 12
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Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                     Producing culturing and heavy
                    The present sequence is that of an anti-CD18 antibody heavy chain including a heat stable enterotoxin II (STII) secretion signal and a C-terminal leucine zipper domain. This recombinant heavy chain is produced by host cells transformed with claimed vector pxCD18-7T3 (see ABZ82071). The plasmid contains 2 translational units that temporally separate the transcription of the antibody light (see ABF72745) and heavy chains. Expression of the light chain is under the control of the phoA promoter, while expression of the heavy chain is under the control of the inducible TacII promoter. In an example from the invention, Escherichia coli 59A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified.
Escherichia coli.
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  transformed with pxCD18-7T3. The light chain was expressed initially
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                                                                                                                                                                                                                                                                     52; Fig 3; 73pp; English.
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                                                                                                                                                                                                                                                                                                                     an antibody for treating cancer or autoimmune diseases the host cell under suitable conditions so that the lic chain are expressed in a sequential fashion.
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/note= "heat stable enterotoxin II (STII)
24. .300
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77.0%;
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No. 5.5
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The H52 antibody ca is for treating for interrupted blood :

This Disclosure;

sequence

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be used in the method of ischaemic stroke, i.e.

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umanised H52 antibody.
invention. The method
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9; 41pp;

English.

Administering an anti-CD18 antibody to treat focal ischaemic stroke increasing cerebral blood flow and reducing size of brain infarct.

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Matches 97
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                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                Humanised antibody; HuH52; heavy chain; focal ischaemic stroke; emboli brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism transfent ischaemic attack; thrombolytic therapy; thrombosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                               Heavy chain of full length
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(UYVB-)
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                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                        systemic hypoperfusion; cardiac arrest.
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77.0%;
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Pred. No. 5.5e
7; Mismatches
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RESULT 14
AAYOB755
ID 0A795
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XX AYOB
XX IGG;
KW IGG4;
KW IGG4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;
IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;
Cerebropyrotective; cerebral artery obstruction; blood flow; infarct;
CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;
Disclosure; Col 31-34; 25pp; English
                                            Anti-CD18 antibodies in stroke.
                                                                                         WPI; 1999-370483/31.
                                                                                                                                                                                                                                                                                                                                                22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   huH52 heavy chain protein fragment.
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77.0%;
                                                                                                                                        Gross CE;
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Pred. No. 8.6e-39;
7; Mismatches 15;
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Best Local
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22-JAN-1997;
17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a method for improving the clinical outcome in focal ischaemic stroke by administering novel anti-CD18 antibody which has cerebroprotective properties. The invention particularly describes a method of treating focal ischaemic stroke caused by the obstruction of a main cerebral artery which comprises administering an anti-CD18 antibody to increase the blood flow or reduce the infarct size, where: (1) the antibody binds to an extracellular domain of CD18 and inhibits or reduces the ability of the cell expressing CD18 to bind to endothelium, (2) the antibody binds CD18 with an affinity of less than 4 nm, or (3) the antibody dissociates CD11b/CD18 complex. This sequence represents the
                                                                                                                                                                                                                                                                                                                                                        Human; humanised H52 antibody; huH52; cerebral blood flow; infa
focal ischaemic stroke; main cerebral artery;
tissue plasminogen activator; anti-CDI8 antibody; stroke;
acute ischaemic stroke; thrombolytic therapy;
Fabvlb salvage receptor binding epitope; thromboembolic stroke
                                                                                                                       Bednar MM,
                                                                                                                                                                                                                                 20-DEC-2000; 2000US-00811384
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                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Full length humanised H52 antibody (huH52), heavy chain.
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97US-00788800.
99US-00251652.
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77.0%;
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Pred. No. 8.6e-39;
7; Mismatches 15;
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                                                                                                                       Gross
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Increasing cerebral blood flow and/or reducing infarct size in focal ischemic stroke using anti-CD18 antibody and tissue plasminogen activator is useful to improve clinical outcome in acute ischemic stroke.

Disclosure; Page 6;

27pp; English

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                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of increasing cerebral blood flow and/ or reducing infarct size in focal ischaemic stroke caused by obstruction of a main cerebral artery in a human, comprising co-administering tissue plasminogen activator and anti-CD18 antibody about 3-5 hours after the stroke. The method is used to improve the clinical outcome in acute ischaemic stroke and to provide an alternative to thrombolytic therapy for treating thromboembolic stroke, particularly where thrombolytic therapy has been unsuccessful or is contra-indicated. The present sequence represents the full length humanised H52 antibody (huH52), heavy chain used in the method of the invention
                                                                                                                                                                                                                                                                                                                             Sequence 450 AA;
  121
                                        114 TVSSAS 119
                                                                            61 NORFMORFTISVDKSTSTAYMOMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV 120
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                                                                                                                                                           NQRFKGRFTISLDKSKRTAYLQMNSLRAEDTAVYYCASWIS------DFFDYWGQGTLV 113
TVSSAS 126
                                                                                                                                                                                                                                                Indels
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